

#5

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PATENT APPLICATION
Attorney Docket No.: 19904-008

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

APPLICANTS : Rouquier *et al.*

SERIAL NUMBER : 09/747,155

EXAMINER : Not Yet Assigned

FILING DATE : December 21, 2000

ART UNIT : 1645

FOR : *NOVEL POLYPEPTIDES AND NUCLEIC ACIDS ENCODING SAME*

August 9, 2001

Boston, Massachusetts

BOX MISSING PARTS

Assistant Commissioner for Patents

Washington, D.C. 20231

**STATEMENT IN SUPPORT OF COMPUTER READABLE
FORM SUBMISSION UNDER 37 C.F.R. § 1.821(f)**

Sir

I hereby state that the content of the paper and computer readable form of the Sequence Listing, submitted in the above-identified application in accordance with 37 C.F.R. § 1.821(c) and 1.821(e), respectively, are the same. No new matter has been added.

Respectfully submitted,

Mathew Pavao
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One Financial Center
Boston, Massachusetts 02111
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Fax: (617) 542-2241

09/747,155-00004

SEQUENCE LISTING



#5

<110> Rouquier, Sylvie
Giorgi, Dominique

<120> Novel Polypeptides and Nucleic Acids Encoding Same

<130> 19904-008 (C009B6834US)

<140> 09/747,155

<141> 2000-12-21

<150> 60/171,746

<151> 1999-12-22

<160> 431

<170> PatentIn version 3.0

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<223> Product = olfactory receptor

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aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc	97
Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr	
20 25 30	
cag gtc tat ttc tcc atg ttt ttt cct att ctg ggc aca cta ctc ctg	145
Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu	
35 40 45	
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Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His	
50 55 60	
tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc	241
Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val	
65 70 75 80	
acg tgg ctc att ggt gtc atg acg tcc ctc ctc cat att tct ctg atg	289
Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met	
85 90 95	
aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc	337
Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys	
100 105 110	
gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac	385
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn	
115 120 125	

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agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc      433
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ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag      481
Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
   145               150               155               160

atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
               165               170               175

cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
               180               185               190

ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
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Val Met Tyr Thr Val Thr Pro
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               20               25               30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Gly Thr Leu Leu Leu
               35               40               45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
50               55               60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65               70               75               80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85               90               95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100              105              110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn

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115              120              125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
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Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145              150              155              160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
              165              170              175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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Val Met Tyr Thr Val Val Thr Pro
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tcttcaggta ggaagtataa agccttctcc acctgcagct ctcacctttc agttgtttgc      540
ttattttatg gaacagccct tggaggggtac ctcagttcag ctgtctctct cccccccagg      600
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aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc      97
Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
      20             25             30

cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg     145
Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
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acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac     193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
      50             55             60

tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc     241
Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
      65             70             75             80

acg tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg     289
Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
      85             90             95

aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc     337
Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
      100            105            110

gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac     385
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
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agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc     433
Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
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ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag     481
Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
      145            150            155            160

atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct     529
Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
      165            170            175

cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac     577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
      180            185            190

ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg     625
Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
      195            200            205

gtg atg tac acg gtg gtt acc ccc                                     649
Val Met Tyr Thr Val Val Thr Pro

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Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
 65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
 85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
 130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

cag gtc tat ttc tcc atg ttt ttt cct att ctg gac aca cta ctc ctg 145
Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tat cac tcc ctg cac 193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His
50 55 60

tac acg gtc atc atg agc ccc cgg ctc tgt gga ctg ctg gtt ctg gga 241
Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
65 70 75 80

tcc tgg tgc atc agt gtc atg ggt tcc ctg ctt gag acc ttg act gtt 289
Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
85 90 95

ttg agg ctg tcc ttc tgc atc aaa atg gaa att cca cac ttt ttt tgt 337
Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys
100 105 110

gat ctt cct gaa gtc ctg aag ctc gcc tgt tct gac acc ttc atc aat 385
Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
115 120 125

aat gta gtg ata tac ttt gca act ggc att ctg gct gtg att ccc ttt 433
Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe
130 135 140

act gga ata ctt ttc tct tac tat aaa att gtt ttc tct gta ctg agg 481
Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg
145 150 155 160

att tcc tca gct ggg gga aag tac aaa gcc ttt tcc acc tgt ggt tcc 529
Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

cac ctc tca atg gtc agc ttg ttc tat ggc acg ggc ctt ggg gtc tat 577
His Leu Ser Met Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

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180          185          190
ctc agt tct gca gct ata cca tct tct agg aca agt ctg gtg gcc tca      625
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gtg atg tac acc atg gtc acc ccc      649
Val Met Tyr Thr Met Val Thr Pro
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Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
      35          40          45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His
      50          55          60

Tyr Thr Val Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
65          70          75          80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
      85          90          95

Leu Arg Leu Ser Phe Cys Ile Lys Met Glu Ile Pro His Phe Phe Cys
      100          105          110

Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
      115          120          125

Asn Val Val Ile Tyr Phe Ala Thr Gly Ile Leu Ala Val Ile Pro Phe
      130          135          140

Thr Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Phe Ser Val Leu Arg
145          150          155          160

Ile Ser Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
      165          170          175

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atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct      529
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              165              170              175

cac ctc tcc gtc gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
              180              185              190

ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg      625
Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
              195              200              205

gtg atg tac acg gtg gtt acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
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              20              25              30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
              35              40              45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
              50              55              60

Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65              70              75              80

Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
              85              90              95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
              100              105              110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
              115              120              125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
              130              135              140

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Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
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 195 200 205

Val Met Tyr Thr Val Val Thr Pro
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 agc ctt caa acc agg agc aag gcc atc tct tat ccc tgc tgc ctg acc 97
 Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
 20 25 30
 cag atg tac ttc ttc cat ttc ttc ggc atc gtg gac agc atc ata atc 145
 Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
 35 40 45
 gcc atg atg gct tat gac cgg ttc gtg gcc atc tgc cac ccg ttg cac 193
 Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac gcc acg atc atg agc cca cgc ctc tgt ggt ctg ctg gtc ggc gtc 241
 Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
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 ccc tgg gcg ttt tcc tgc ttc atc tct ctc acc cac atc ctc ctg atg 289
 Pro Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
 85 90 95
 gcc cgc ctc gtt ttc tgc ggc agc cac gag gtg cct cac tac ttc tgc 337
 Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys
 100 105 110
 gac ctc act ccc atc ctc cga ctt tcg tgc aca gac aca tca gtg aac 385
 Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn

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115              120              125
agg atc ttc atc ctc att gtg gca ggg atg gtg ata gcc acg ccc ttc      433
Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
130              135              140

atc tgc atc ctg gct tcc tat gct cgc atc ctt gcg gcc atc atg aag      481
Ile Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Ala Ala Ile Met Lys
145              150              155

gtc ccc tct gca ggc ggc agg aag aaa gcc ttc tcc acc tgc agc tcc      529
Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
165              170              175

cac ctg tct gtg gtt gct ctc ttc tat ggg acc acc att ggt gtc tat      577
His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180              185              190

ctg tgt ccc tcc tcg gtc cgc acg gct gtg aag gag aaa gct tct gcc      625
Leu Cys Pro Ser Ser Val Arg Thr Ala Val Lys Glu Lys Ala Ser Ala
195              200              205

gtg atg tac aca gca gtc acc ccc      649
Val Met Tyr Thr Ala Val Thr Pro
210              215

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Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Ile Ile Ile
35              40              45

Ala Met Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50              55              60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Val
65              70              75              80

Pro Trp Ala Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
85              90              95

Ala Arg Leu Val Phe Cys Gly Ser His Glu Val Pro His Tyr Phe Cys
100             105             110

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Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
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Arg Ile Phe Ile Leu Ile Val Ala Gly Met Val Ile Ala Thr Pro Phe
 130 135 140

Ile Cys Ile Leu Ala Ser Tyr Ala Arg Ile Leu Ala Ala Ile Met Lys
 145 150 155 160

Val Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
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Val Met Tyr Thr Ala Val Thr Pro
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 tgcttcaatg atgtggaaat ctctaaattt ttctgtgacc cttctcaact tctcaatcct 360
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 <223> Taxon = 9557; gene = PPA68; Accession DDBJ/EMBL/GenBank = AF127821

<400> 14
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 1 5 10 15

Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val
 85 90 95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
 145 150 155 160

Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 15
<211> 649
<212> DNA
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9557; gene = PPA72; Accession DDBJ/EMBL/GenBank = AF127822

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 15
c ttc ata gac atc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg 49
Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aac atc cag aca cag agc aga gtc atc acc tat gca ggc tgc atc acc 97
Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
20 25 30

cag atg tgc ttt ttc ata ttc ttt gcg gga ctg gat atc ttt atg ctg 145
Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
35 40 45

acc gtg atg gcc ttt gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193
Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac acg gtc acc atg aac ccc aag ctc tgt ggg ctg ctg gtt ctg gcg 241
Tyr Thr Val Thr Met Asn Pro Lys Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

tcc tgg atc atg aat gcc ctg aat tcc tcg tta caa agc tta ata gtg 289
Ser Trp Ile Met Asn Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa att ccc cac ttt ttc tgt 337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

gaa ctt aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat 385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

gac atg ggg atg tat atg gca tct gct ctg ctg ggc ggt ggt gcc ctc 433
Asp Met Gly Met Tyr Met Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
130 135 140

tct ggg atc ctt tat tct tat tct aag atc ctt tcc tcc ata cgt gga 481
Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Leu Ser Ser Ile Arg Gly
145 150 155 160

acc tcg tca gct cag ggg aag tac aag gca ttt tcc acc tgt gca tct 529
Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

cac ctc tcg gtt gtc tct tta ttt tat ggt acg ctc cta gga gtg tac 577

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

ttt agt tct gct gca act cgt aac tca cac tca agt gct gca gcc tcg 625
 Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

gtg atg tac acg gtg gtt acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 16
 <211> 216
 <212> PRT
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9557; gene = PPA72; Accession DDBJ/EMBL/GenBank = AF127822

<400> 16
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Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30

Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
 35 40 45

Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Thr Met Asn Pro Lys Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Ile Met Asn Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

Asp Met Gly Met Tyr Met Ala Ser Ala Leu Leu Gly Gly Gly Ala Leu
 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Leu Ser Ser Ile Arg Gly
 145 150 155 160

Thr Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 17
 <211> 649
 <212> DNA
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9557; gene = PPA79; Accession DDBJ/EMBL/GenBank = AF127823

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 17
 c ctt gtc gat gtc tcc tat gcc aca agc ata gtc cct cag ctg ctg gca 49
 Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala
 1 5 10 15
 cat ttt ctt gca gaa cat aaa gcc atc tcg ttg cag agc tgt gca gcc 97
 His Phe Leu Ala Glu His Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala
 20 25 30
 caa tta ttt ttc tcc ctg gcc ttg ggt ggg att gag ttt gtt ctc ctg 145
 Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
 35 40 45
 gca gtg atg gcc tat gac cgc tat gtg gct gtg tgt gac ccc ctg cga 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg
 50 55 60
 tac tca gcc acc atg cat gga gcg cta tgt gct aag ttg gcc atc aca 241
 Tyr Ser Ala Thr Met His Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr
 65 70 75 80
 tcc tgg gtc agt gga tcc att aac tct ctc atg cat acc acc atc acc 289
 Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Met His Thr Thr Ile Thr
 85 90 95
 ttt cag ctg ccc atg tgc aca aac aag ttt att aat cat ata ttc tgt 337
 Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asn His Ile Phe Cys
 100 105 110
 gaa att cta gct gtg atc agg ctg gct tgt gtg gac acc tcc tcc aac 385
 Glu Ile Leu Ala Val Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn
 115 120 125
 gag gtc acc atc atg gtg tct agc att gtt ctt ctg atg aca ccc tta 433
 Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Leu
 130 135 140
 tgt ctg gtt ctt ttg tct tac atc cgg atc atc tcc acc atc tta aag 481

Cys Leu Val Leu Leu Ser Tyr Ile Arg Ile Ile Ser Thr Ile Leu Lys
 145 150 155 160

atc cag tcc aga gaa gga agg agg aaa gcc ttc cac acg tgt gcc tct 529
 Ile Gln Ser Arg Glu Gly Arg Arg Lys Ala Phe His Thr Cys Ala Ser
 165 170 175

cac ctc aca gtg gtt gcc ctg tgc tat ggc atg gcc att ttc act tac 577
 His Leu Thr Val Val Ala Leu Cys Tyr Gly Met Ala Ile Phe Thr Tyr
 180 185 190

atc cat ccc cac tcc agt ccc tct gtc ctt cag gag aag ttg atc tct 625
 Ile His Pro His Ser Ser Pro Ser Val Leu Gln Glu Lys Leu Ile Ser
 195 200 205

ctc ttt tat gcc att ttg aca cca 649
 Leu Phe Tyr Ala Ile Leu Thr Pro
 210 215

<210> 18
 <211> 216
 <212> PRT
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9557; gene = PPA79; Accession DDBJ/EMBL/GenBank = AF127823

<400> 18
 Leu Val Asp Val Ser Tyr Ala Thr Ser Ile Val Pro Gln Leu Leu Ala
 1 5 10 15

His Phe Leu Ala Glu His Lys Ala Ile Ser Leu Gln Ser Cys Ala Ala
 20 25 30

Gln Leu Phe Phe Ser Leu Ala Leu Gly Gly Ile Glu Phe Val Leu Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asp Pro Leu Arg
 50 55 60

Tyr Ser Ala Thr Met His Gly Ala Leu Cys Ala Lys Leu Ala Ile Thr
 65 70 75 80

Ser Trp Val Ser Gly Ser Ile Asn Ser Leu Met His Thr Thr Ile Thr
 85 90 95

Phe Gln Leu Pro Met Cys Thr Asn Lys Phe Ile Asn His Ile Phe Cys
 100 105 110

Glu Ile Leu Ala Val Ile Arg Leu Ala Cys Val Asp Thr Ser Ser Asn
 115 120 125

Glu Val Thr Ile Met Val Ser Ser Ile Val Leu Leu Met Thr Pro Leu
 130 135 140


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Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala Asp Thr Ala Leu Phe
    115                      120                      125

gag atc tac gcc atc gtc gga acc att ctg gtg gtc atg atc ccc tgc      433
Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro Cys
    130                      135                      140

ttg ctg atc ttg tgt tcc tat act cgc att gct gct gcc atc ctc aag      481
Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu Lys
    145                      150                      155                      160

atc cca tca gct aaa ggg aag aat aaa gcc ttt tct aca cgt tcc tca      529
Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser
    165                      170                      175

cac ctc ctt gtt gtc tct ctt ttc tat ata tca tta agc ctc aca tat      577
His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr Tyr
    180                      185                      190

ttt cgg cct aaa tca aat aat tct cct gag ggc aag aag ctg cta tcg      625
Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu Ser
    195                      200                      205

ttg tcc tac act gtt atg act ccc      649
Leu Ser Tyr Thr Val Met Thr Pro
    210                      215

<210> 20
<211> 216
<212> PRT
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9598; gene = PTR12; Accession DDBJ/EMBL/GenBank = AF127824

<400> 20
Phe Leu Glu Ile Gly Phe Asn Leu Val Ile Val Pro Lys Met Leu Gly
1                      5                      10                      15

Thr Leu Leu Ala Gln Asp Thr Thr Ile Ser Phe Leu Gly Cys Ala Thr
    20                      25                      30

Gln Met Tyr Phe Phe Phe Phe Phe Gly Val Ala Glu Cys Phe Leu Leu
    35                      40                      45

Ala Thr Val Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
    50                      55                      60

Tyr Pro Val Ile Met Asn Gln Arg Thr Arg Ala Lys Leu Ala Ala Ala
    65                      70                      75                      80

Ser Trp Phe Pro Gly Phe Pro Val Ala Thr Val Gln Thr Thr Trp Leu
    85                      90                      95

Phe Ser Phe Pro Phe Cys Arg Thr Asn Lys Val Asn His Phe Phe Cys
    100                      105                      110

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Asp Ser Pro Pro Val Leu Arg Leu Val Cys Ala Asp Thr Ala Leu Phe
 115 120 125

Glu Ile Tyr Ala Ile Val Gly Thr Ile Leu Val Val Met Ile Pro Cys
 130 135 140

Leu Leu Ile Leu Cys Ser Tyr Thr Arg Ile Ala Ala Ala Ile Leu Lys
 145 150 155 160

Ile Pro Ser Ala Lys Gly Lys Asn Lys Ala Phe Ser Thr Arg Ser Ser
 165 170 175

His Leu Leu Val Val Ser Leu Phe Tyr Ile Ser Leu Ser Leu Thr Tyr
 180 185 190

Phe Arg Pro Lys Ser Asn Asn Ser Pro Glu Gly Lys Lys Leu Leu Ser
 195 200 205

Leu Ser Tyr Thr Val Met Thr Pro
 210 215

<210> 21
 <211> 650
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(650)
 <223> Taxon = 9598; gene = PTR2; pseudogene; Accession DDBJ/EMBL/ GenBank =
 AF127825

<400> 21
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 cgggactcag accatctcct tctgtggctg tttcacacag atgtatttcg ttttcatgct 120
 tgtggacatg gacaatttcc tcctagctgt gatggcctat gaccgctttg tcgccgtgtg 180
 ccacccctta cattacacag caaagatgac ccatcagctc tgtgccctgc tggttgctgg 240
 attatgggtg gttgccaacc tgaatgtcct tctgcacacc ctgctgatgg ctcgactctc 300
 attctgtgca gacaatgcca tccctcactt cttctgcgat gtgactcccc tactgaaact 360
 ctctgtctca gacacacacc tcaatgaggt cataatcctt agtgagggtg ccctggtcac 420
 gatcacccca tttcttttgc tcttggtctc ttatatgcac atcacctgca ctgtcctgag 480
 ggtcccatcc acaaaggga ggtggtaagc cttctccacc tgtggctctc acctggctgt 540
 ggttctacct cttctatggc accatcattg ctgtgtatct taacctctg tcctccact 600
 cagcagagaa agacactacg gctactgtgt tgtatacagt agtgactccc 650

<210> 22
 <211> 649

<212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9598; gene = PTR3; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127826

<400> 22
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 ggaagacaga accatctcct tcacaggatg catcatgcaa ttcttctcgg cgtgtatatg 120
 tgcagtggca gaaacattca tgctggcagt gatggcctat gattgatacg tggcagtgtg 180
 taaccctttg ctctacacag ttgtcaggtc ccagaaactc tgtgcatcat tagtggcagg 240
 gccctacaca tgggggtataa totcttctct gacactcacc tatttctctt tgtcattatc 300
 cttctgtggg tctaacatca tcaataatth tgtctgtgag gactctgtca tcctctctgt 360
 ctctgtctct gacccttaca tcagccaaat gctttgtttt gtcattgcaa tattcaatga 420
 ggtgagcagc ttgggagtc tctcactac ctatatthtc atctttattg ctgtcataaa 480
 aatgccttct gctgttgggc accaaaaagc tttctctacc tgtgcttccc acctgactgc 540
 catcactatt ttccatggga ctgtcctgtt cctttattgt gtacccaact ccaaaaaactc 600
 atggctcata gtcaaagtag gttctgtgtt ttatacagtc atcatcccc 649

<210> 23
 <211> 651
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(651)
 <223> Taxon = 9598; gene = PTR4; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127827

<400> 23
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 tggaggatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca 180
 tctgtcacct atatcgttca gccatcttta acccgtgttt ctgtggcttc ctagatttgt 240
 tgtctttttt ttttttctca gtctttcaga ctcccagctg cacaacttga ttgccttaca 300
 aatgacctgc ttcaaggatg tggaaattcc taatttcttc tgggaacctt ctcaactctc 360
 ccctcttgca tgttgtgaca ccttcaccag gaacatcagt atttccctgc tgccatattt 420
 ggttttcttc ctatctcaca gatcattttc tcttactata aaattgtttc ctccatgctg 480
 agtgtttcat catcagggtg gaagtataaa gccttctcca actgtgggtc tcccctgtca 540
 gttgtttgct tattttatgg gaaaggcatt ggggggtacc tgagttcaga tgtgtcatct 600
 tccccagaa aggggtgcagt ggctcagtg atgtacacgg tgatcaccgc c 651

<210> 24
 <211> 657
 <212> DNA
 <213> Pan troglodytes

 <220>
 <221> misc_feature
 <222> (1)..(657)
 <223> Taxon = 9598; gene = PTR5; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127828

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<400> 24
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tcacagcaga ctcatctcct aggcaggctg cctgactccg atgtccctct ttgccatttt    120
tgaggagcatg gaagagagac atgctcctga gtgtgatggc ctattaccgg tttgtggcca    180
tctgtcaccg tatatatcat tcaaccatca tgaaccctg tttctgtggc tttctagttt    240
tggtgtcttt ttttttttct cagtctttta gacgccagc tgcacaactt gattgcctta    300
caaatgacct gcttcaagga tgtggaaatt cctaatttct tctgggaacc ttctcaactt    360
cccatcttg catgttgca caccctcacc aataacataa tcatgtattt cctgctgcc      420
atatttggtt ttcttcccat ctgggggacc cttttctctt attataagat tgtttcctcc    480
attctgaggg tttcatcatc aggtgggaag tataaggcct gctccacctg tgggtctcac    540
ctgtcagttg tttgctgatt ttatggaaga tgcgttggag ggtacctcag ttcagatgtg    600
tcatcttccc tgagataggg tgcagtggcc tcagtgatgt acacggtggt caccccc      657
  
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<210> 25
 <211> 657
 <212> DNA
 <213> Pan troglodytes

 <220>
 <221> misc_feature
 <222> (1)..(657)
 <223> Taxon = 9598; gene = PTR6; pseudogene; Accession DDBJ/EMBL/GenBank = AF127829

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<400> 25
cttgctgac atcagtttca cctccatcac agtccccaag atgattgtgg acatctagtc      60
tcacagcaga gtcactgct atgcagggtg cctgactcag atgtctctct ttgccatttt    120
tgaggagcatg gaagagagac atgctcctga atgtgatggc ctatgtccgg tttgtagcca    180
tctgtcaccg tctatatcat tcagccatca tgaaccctg tttctgtggc ttcctacttt    240
tggtgtcttt ttttttttct ggggtctttt agatgccag ctgcacaaca tgattgcctt    300
acaaacgacc tgcttcaagg atgtggaaat tcctaatttc ttctgtgac cttctcaact    360
acccacctt gcatgttgtg acaccttcac caataacatc atcatgtatt tccctgctgc    420
cctatttggt ttcttccca tctgggggac cttttctct tactgtaaaa ttgtttcctc    480
cattctgagg gtttcatcat caggtgggaa gtataaacct tctccacctg tgggtctcac    540
  
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tgtgtgccata tttgggttttc ttcccatctc ggggaccctt ttctcttact gtaaaattgt 480
ttctctcatt ctgagggttt catcatcagg tgggaagtat aaaccttcac cacttggtgg 540
ttcacctgt cagttgtttg ctgattttat ggaacaggcg ttggagggta cctcggttca 600
gatgtgtcat cttccccgag aaaggggtgca gtggcctcag tgatgtacac ggtggtcacc 660
ccc 663
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<210> 28
<211> 677
<212> DNA
<213> Pan troglodytes
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<220>
<221> misc_feature
<222> (1)..(677)
<223> Taxon = 9598; gene = PTR9; pseudogene; Accession DDBJ/EMBL/Genbank =
AF127832
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<400> 28
cttgactgac atcgggtttca cctccatcac agtccccaag atgattgtgg acatctagtc 60
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tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatggccgg tttgtagcca 180
tctgtcacc tccatatact tcagccattt tgaaccctg tttctgtggc ttcttagatt 240
tgttgtcctt gttttttttt gttttgtttt gtttttttct caggctttta gactcccagc 300
tgcacaactt gattgcctta caaatgacgt gtttcaagga tgtggaaatt cctaatttct 360
tctgggaacc ttctcaactc gccatcttg catgtgttaa caccttcacc aggaatatca 420
acctgtattt cctgtctgcc gtatttggtt ttcttccat ctcggggacc cttttctctt 480
actgtaaaat tgtttcctcc attctgaagg ttcatcatc aggtgggaac tataaagcct 540
tctccacctg tgggtctcac ctgtcagttg ttgcttatt ttatggaaca ggcgttggag 600
ggtacctcag ttcagatgtg tcattctccc ccagaaaggg tgcagtggcc tcagtgatgt 660
acacggtggt caccccc 677
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<210> 29
<211> 643
<212> DNA
<213> Hylobates lar
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<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 9580; gene = HLA45; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127833
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<400> 29
ctgggtgac atcactttca cctcggccat ggttcccaag atggttgtgg acatgcagtc 60
gcatagcaga gccatctctt atgcaggctg cctgacacag atgtctttct ttgtcctttt 120
gcatgtatag aagacatgct cctgactctg atggcctatg accgatttgt ggccatctgt 180
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cacccccctgc actaccagct catcgtgaat cctcacctct gtgtcttctt agttttgttg 240
tcttttttcc ttagcctggt ggattcccag ctacacagct ggattgtggt tacaattcac 300
cttcttcaag aatggaaatc tctaattttt tctgtgacct gtctcaactt ctcaaccttg 360
cctgttctga cagcatcatc gataacatat tatatattta gatagcccta tatttggttt 420
tcttcccatt tcagggatcc ttttgtctta gtataaaatt gtctcccca ttccgagaat 480
tccatcatca gatgggaagt ataaagcctt ctccacctgt ggctctcacc tggcagttgt 540
tgcattttat gaaacaggca ttggcggtga cctgaactta gctgtgtcat catccccag 600
gaatggtgtg gtggcgctcag tgatgtatgc tgtggtcacc ccc 643

<210> 30
<211> 648
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 9580; gene = HLA46; pseudogene; Accession DDBJ/EMBL/GenBank = AF127834

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acagactcaa tccatcagtt acacaggctg cctcaccxaa atctgctttg tcttggtttt 120
tgttggttg gaaaatggaa ttctgggtcat gatggcctat gatcgatttg tggccatctg 180
tcacccactg aggtacaatg tcatcatgaa cccaaactct gtgggctgct gcttctgctc 240
tccttcatca ttagtgtcct ggacgctctg ctgcacacgt tgatgggtgct acggctgacc 300
ttctgcacag acctggaaat tccccacttt ttctgtgaac tagctcatgt tctcaagctc 360
gcctgttctg atgtcctcat taataacatc ctgggtgtatt tggtgaccgg cctgttaggt 420
gttgttcctc actctgggat cattttctct tacacacgaa ttgcctcctc tgtcatgaaa 480
attccattag ctgggtggaaa gtataaagct ttttccatct gggggtcaca cttaatcgtc 540
gtttgcttgt tctatggaa acgggtttggg gtgtacctta gttctggggc taccactcc 600
tctaggcagg gtgcaatagc atcagtgatg tataccgtgg tcaccccc 648

<210> 31
<211> 660
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(660)
<223> Taxon = 9580; gene = HLA47; pseudogene; Accession DDBJ/EMBL/GenBank = AF127835

<400> 31
ctgcctgac atcggtttca cttccaccac agtccccaag attattgtgg acatcaaac 60


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gaa ctg aca cac atc ctc cag ctg gcc cgc tct gat acc ttc ctg aac      385
Glu Leu Thr His Ile Leu Gln Leu Ala Arg Ser Asp Thr Phe Leu Asn
      115                      120                      125

agc acg ttg ata tac ttt atg aca ggt gtg ctg ggc gtt ttt ccc ctc      433
Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
      130                      135                      140

ctt ggg atc att ttc tct tat tca cga att gct tca tcc ata agg aag      481
Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
      145                      150                      155                      160

atg tcc tca tct ggg gga aaa caa aaa gca ctt tcc acc tgt ggg tct      529
Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
      165                      170                      175

cac ctc tcc gtt gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
His Leu Ser Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
      180                      185                      190

ttc act tct gca gtg act cac gct tcc cag aaa atc tcc gtg gcc tcg      625
Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
      195                      200                      205

gtg atg tac act gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Pro
      210                      215

<210> 33
<211> 216
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA48; Accession DDBJ/EMBL/GenBank = AF127836

<400> 33
Trp Val Asp Ile Cys Phe Gly Thr Cys Ile Ile Pro Lys Met Leu Val
1          5          10          15

Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
      20          25          30

Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
      35          40          45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50          55          60

Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
      65          70          75          80

Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
      85          90          95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
      100          105          110

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Glu Leu Thr His Ile Leu Gln Leu Ala Arg Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 34
<211> 649
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA5; Accession DDBJ/EMBL/GenBank = AF127837

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 34
c tgg gtt gac atc tgt ttc agc act tgc atc atc ccc aag atg ctg gtg 49
Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Ile Pro Lys Met Leu Val
1 5 10 15

aac atc cag acc aag aac aaa gcc atc tcc tac atg gac tgc ctc aca 97
Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

cag gtc tat ttc tcc atg ctt ttt cct att ctg gac acg cta ctc ctg 145
Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc ctc cct ctg cac 193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His
50 55 60

tac atg atc atc atg aac ccc cgc ctc tgt ggc ctc ctg att ttt gtc 241
Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
65 70 75 80

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atc tgg ctc att ggt gtc atg aca tcc ctc ctc cat att tct ctg atg      289
Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
                        85                        90                        95

atg cat cta atc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc      337
Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
                        100                        105                        110

gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac      385
Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
                        115                        120                        125

agc acg ttg ata tac ttt atg aca ggt gtg ctg ggc gtt ttt ccc ctc      433
Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
                        130                        135                        140

ctt ggg atc att ttc tct tat tca cga att gct tca tcc ata agg aag      481
Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145                        150                        155                        160

atg tcc tca tct ggg gga aaa caa aaa gca ctt tcc acc tgt ggg tct      529
Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
                        165                        170                        175

cac ctc tcc gtt gtt tct tta ttt tat ggg aca ggc att ggg gtc cac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
                        180                        185                        190

ttc act tct gca gtg act cac gct tcc cag aaa atc tcc gtg gcc tcg      625
Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
                        195                        200                        205

gtg atg tac acg gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
210                        215

<210> 35
<211> 216
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA5; Accession DDBJ/EMBL/GenBank = AF127837

<400> 35
Trp Val Asp Ile Cys Phe Ser Thr Cys Ile Ile Pro Lys Met Leu Val
1                        5                        10                        15

Asn Ile Gln Thr Lys Asn Lys Ala Ile Ser Tyr Met Asp Cys Leu Thr
20                        25                        30

Gln Val Tyr Phe Ser Met Leu Phe Pro Ile Leu Asp Thr Leu Leu Leu
35                        40                        45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys Leu Pro Leu His
50                        55                        60

Tyr Met Ile Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Ile Phe Val
65                        70                        75                        80

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Ile Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met
85 90 95

Met His Leu Ile Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Phe Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Gln Lys Ala Leu Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
180 185 190

Phe Thr Ser Ala Val Thr His Ala Ser Gln Lys Ile Ser Val Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 36
<211> 651
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(651)
<223> Taxon = 9580; gene = HLA6; pseudogene; Accession DDBJ/EMBL/GenBank = AF127838

<400> 36
cttgccctgac atcggtttca ccaccaccac ggtccccgag atgattgtgg acatccaatc 60
tcacagcaga gtcattctct aggcaggccg cctgactcac atgtctctct ttgccatttt 120
tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgacagg tttgtagcca 180
tctgtcacc cctatatcat tcagccatca tgaacccgtg tttctgtggc tttctagttg 240
tctttttttt ctctcagtct tttagaggcc cagctgcata acttgattgc cttgctaattg 300
acctgcttca aggatgtgga aattcctaata ttcctctgtg acccttctca actccgccat 360
cttgcatggt gtgacatctt caccaataac ataatcatgt attttctctg tgccgtattt 420
gggttccttc ccatctcggg gaccctttcc tcttactata aaatggtttc ctccattctg 480

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aggctttcat cgtcagggtgg gaagtataaa gccttctcca cctgtgggtc tcacctgtca      540
gttgtttgct gagtttatgg aagaggcggt ggagggtacc tcagttcaga tgtgtcctct      600
tccccagaa agtttgagcgt ggcctcagtg atgtacacgg tggtcacccc c                651

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<210> 37
<211> 644
<212> DNA
<213> Hylobates lar

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<220>
<221> misc_feature
<222> (1)..(644)
<223> Taxon = 9580; gene = HLA7; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127839

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<400> 37
ctgggctgac atcactttca cctcggccat gggtcccaag atgattgtgg acatgcagtc      60
gcatagcaga gccatctctt atgcaggctg cctgacacag atgtctttct ttgtcctttt      120
tgcattgtatg gaagacatgc tcctgactct gatggcctat gaccgatttg tggccatctg      180
tcaccccttg cactaccag tcacgtgaa tcctcacctc tgtgtcttct tagttttgtt      240
gtcttttttc cttagcctgt tggattccca gctacacagc tggattgtgt ttacaatcca      300
ccttcttcaa gaatggaaat ctctaatttt ttctgtgacc cgtctcaact tctcaacctt      360
gcctgttctg acagcatcat cgataacata ttatatattt agatagccct atatttggtt      420
ttcttcccat ttcagggatc cttttgtctt agtataaaat tgtctcccc attctgagaa      480
ttccatcgtc agatgggaag tataaagcct tctccacctg tggctctcac ctggcagttg      540
ttgcatttta tgaacaggc attggcgtgt acctgacttc agctgtgtca tcatccccc      600
ggaatggtgt ggtggcgtca gtgatgtatg ctgtggtcac cccc                        644

```

```

<210> 38
<211> 649
<212> DNA
<213> Hylobates lar

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<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA74; Accession DDBJ/EMBL/GenBank = AF127840

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<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

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<400> 38
c ttt gtt gat ttc tgt tat tct act acg att aca ccc aaa ctg ctg gag      49
Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
1          5          10          15

aac ttg gtt gtg gaa tat aga act att tcc ttc aca gga tgc atc atg      97
Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
20          25          30

```

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caa ttc ttc ctt gtc tgc ata ttt gta ggg aca gaa aca ttc atg ctg      145
Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu
      35                      40                      45

gca gtg atg gcc tat gac cga tgt gtg gcg gtg tgt aac cct ctt ctc      193
Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu
      50                      55                      60

tac aca gtt gca atg tcc cag agg ctt tgc tcc ttg ttg gtg gct aca      241
Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
      65                      70                      75                      80

tca tac tct tgg ggg ata gtc tgt ttc ctg aca ctt acc tac ttt cta      289
Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu
      85                      90                      95

ctg gaa tta tcc ttc aga gga aat aat atc att aat aac ttt gtc tgt      337
Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
      100                      105                      110

gag cat gct gcc att gtt gct gtg tct tgc tct gac ccc tat gtg agc      385
Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser
      115                      120                      125

cag gag atc act tta gtt tct gcc aca ttc aat gaa ata agc agt ctg      433
Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
      130                      135                      140

atg atg att ttc act tcc tat gct ttc att ttt atc act gtc atg aag      481
Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
      145                      150                      155                      160

atg cct tcc act ggg ggg cgc aag aaa gcg ttc tcc acg tgt gcc tcc      529
Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
      165                      170                      175

cac ctg acc gcc att acc att ttc cat ggg act atc ctt ttc ctc tac      577
His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
      180                      185                      190

tgt gtt cct aac tcc aaa agt tca tgg ctc atg gtc aag gtg acc tct      625
Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Thr Ser
      195                      200                      205

gtc ttt tac aca gtg ttc att ccc
Val Phe Tyr Thr Val Phe Ile Pro
      210                      215

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<210> 39
<211> 216
<212> PRT
<213> Hylobates lar

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<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9580; gene = HLA74; Accession DDBJ/EMBL/GenBank = AF127840

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<400> 39
Phe Val Asp Phe Cys Tyr Ser Thr Thr Ile Thr Pro Lys Leu Leu Glu
1                      5                      10                      15

```

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Asn Leu Val Val Glu Tyr Arg Thr Ile Ser Phe Thr Gly Cys Ile Met
      20                      25                      30

```

Gln Phe Phe Leu Val Cys Ile Phe Val Gly Thr Glu Thr Phe Met Leu
 35 40 45

Ala Val Met Ala Tyr Asp Arg Cys Val Ala Val Cys Asn Pro Leu Leu
 50 55 60

Tyr Thr Val Ala Met Ser Gln Arg Leu Cys Ser Leu Leu Val Ala Thr
 65 70 75 80

Ser Tyr Ser Trp Gly Ile Val Cys Phe Leu Thr Leu Thr Tyr Phe Leu
 85 90 95

Leu Glu Leu Ser Phe Arg Gly Asn Asn Ile Ile Asn Asn Phe Val Cys
 100 105 110

Glu His Ala Ala Ile Val Ala Val Ser Cys Ser Asp Pro Tyr Val Ser
 115 120 125

Gln Glu Ile Thr Leu Val Ser Ala Thr Phe Asn Glu Ile Ser Ser Leu
 130 135 140

Met Met Ile Phe Thr Ser Tyr Ala Phe Ile Phe Ile Thr Val Met Lys
 145 150 155 160

Met Pro Ser Thr Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Leu Thr Ala Ile Thr Ile Phe His Gly Thr Ile Leu Phe Leu Tyr
 180 185 190

Cys Val Pro Asn Ser Lys Ser Ser Trp Leu Met Val Lys Val Thr Ser
 195 200 205

Val Phe Tyr Thr Val Phe Ile Pro
 210 215

<210> 40
 <211> 659
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(659)
 <223> Taxon = 9580; gene = HLA75; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF127841
 <400> 40
 cttgcctgac atcggtttca ccaccaccac ggtccccgag atgattgtgg acatccaatc 60
 tcacagcaga gtcacatcct aggcaggccg cctgactcag atgtctctct ttgccatttt 120

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tggaggcatg gaagagagac atgctcctga gtgtgacggc ctatgaccgg tttgtagcta 180
tctgtcaccc tctatatcat tcagccatca tggaccctgt tttctgtgac ttcctagttt 240
tgttgtcttt tttttttctt ctcagtcttt tcgactccca gctgcacaac ttgattgcct 300
tgctaatagac ttgcttcaag gatgtggaaa ttcctaattt cttctgtgac cttctcctcaac 360
tcccccatct tgcattgtgt gacagcatca ccaataacgt catcatgtat ttcctctgtg 420
ccgtatttgg tttccttccc atctcgggga cccttttctc ttgctataaa atcgtttcct 480
ccattctgag ggtttcatca tcaggtggga ggtataaagc cttctccacc tgtgggtctc 540
acctgtcagt tgtttgtctga gtttatggaa gaggtgttgg aggggtacctc agttcagggtg 600
tgtcatcttc cccagaaaag ggtgcagtgg cctcagtcat gtacacgggtg gtcaccccc 659
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<210> 41
<211> 662
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(662)
<223> Taxon = 9580; gene = HLA8; pseudogene; Accession DDBJ/EMBL/ GenBank =
AF127842
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<400> 41
gtcacctgac gtcgggtttca cctccaccac ggtccccgag atgattgtgg acaccatttc 60
tcacagcaca gtcattctct aggagggctg cctgactcag atgcctctct ttgccatttt 120
tggaggcatg gaagagagac aagctcctga gtgtgatggc ctatgaccgg tttgtagcca 180
tctgtcaccc tctatatcgt tcagccatca tgaatccgtg tttctgtggc tacctagttt 240
tgttgtcttt ttttttttct ttcgcagtcg ttttagactcc cagctgcaca acttgattgc 300
cttgctaata acctgcttca gggatgcgga aattcctaata ttcttctgtg acccttctca 360
actcccccat cttgcatggt gtgacacctt caccaataac ataatacatgt tatttccttg 420
ctgccatatt tggtttctct cccatctcgg ggacctttt ctctttctgt aaaattgttt 480
cctccgttct gaggggtttca tcgtcaggta ggaagtataa agccttctcc acctgtgggt 540
ctcacctgtc agttgtttgc tgagtttatg gaagaggcgt tggaggggtac gtcagttcag 600
atgtgtcttc tccccccaga aagggtgcag tggcctcagt gatgtacatg atggtcaccc 660
cc 662
```

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<210> 42
<211> 662
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(662)
<223> Taxon = 9593; gene = GG01; pseudogene; Accession DDBJ/EMBL/ GenBank =
AF127843
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<400> 42
cttgactgac atcgggtttca cctccaccac agtccccaag atgattgtgg acatccagtc      60
tcacagcaga gccatctcct atgcacgctg cctgactcag atgtctctct ttgccatttt      120
tgaggagcatg gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca      180
tctgtcacc cctgtatcgt ccagccatct tgaacccctg tttctgtggc ttcctagatt      240
cgttgtcctt gttttttttt tttttttctc agtccttttag actcccagct gcacaacttg      300
attgccttac aaatgacctg cttcatggat gtggaaattc ctaatttctt ctgggaacct      360
tctcaactcc cccatcttgc atgttgtgac accttcacca ggaacatcaa cctgtatttc      420
cctgctgcca tatttggttt tcttccatc tcggggaccc ttttctctta ctataaaatt      480
gtttcctcca ttctgaaggt ttcacaggt gggaagtata aaccttctcc gcctgtggtt      540
ctcacctgtc agttgtttac tgattttatg gaacaggcgt tggagggtac ctcggttcag      600
atgtgtcatc ttccccgaga aagggtgcag tggcctcagt gatgtacacg gtggtcacc      660
cc                                                                                   662
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<210> 43
<211> 650
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 9593; gene = GG017; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127844
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<400> 43
ttttgctgac ctctgtttta cctccacgac tgtcccaaag atgttactga atatactgac      60
acagaacaaa ttcataacat atgcaggctg tctcggtcag attttttttt ttcacttcat      120
ttggatgcct ggacaattta ctcttgactg tgatggccta tgaccgcttc gtggccatct      180
gtcaccacct gcactatacg gtcacatga acccccggt ctgtggactg ctggttctgg      240
ggtcctggtg catcagtgtc atgggttccc tgctcgagac cttgactgtt ttgaggctgt      300
ccttctgcac caaaatggaa attccacact ttttttgtga tcttcttgaa gtctgaagc      360
tcgcctgttc tgacaccttc attaataacg tgggtgatata ctttgcaact ggcgtcctgg      420
gtgtgattcc cttcactgga atatttttct cttactataa aattgttttc tctatactga      480
ggatttctc agctgggaga aagcacaagg cgttttccac ctgtggttcc cacctctcag      540
tggtcacctt gttctatggc acgggctttg gggctctatc cagttctgca gccacaccat      600
cttctaggac aagtctggtg gcctcagtga tgtacaccat ggtcaccccc      650
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<210> 44
<211> 649
<212> DNA
<213> Gorilla gorilla
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<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9593; gene = GGO18; Accession DDBJ/EMBL/GenBank = AF127845

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 44
 c ttc gta gac atc tgt ttt gtc tct acc act gtc ccg aag atg ctg gtg 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag aca cac aac aaa gtc atc acc tat gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30
 cag atg tgc ttt ttc tta ctc ttt gta gga ttg gat aac ttc ctt ctg 145
 Gln Met Cys Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu
 35 40 45
 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac cct ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac atg gtc att atg aac cct caa ctc tgt gga ctg ctg gtt ctg gcg 241
 Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80
 tcc tgg atc gtg ggt gtt ctg aat tcc atg tta caa agc tta atg gtg 289
 Ser Trp Ile Val Gly Val Leu Asn Ser Met Leu Gln Ser Leu Met Val
 85 90 95
 ttg cca ctg ccc ttt tgt aca cac atg gaa atc cct cat ttt ttc tgt 337
 Leu Pro Leu Pro Phe Cys Thr His Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 gaa att aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat 385
 Glu Ile Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125
 gac ata gtg atg tat ttt gca gta gca ctg ctg ggc ggt ggt ccc ctc 433
 Asp Ile Val Met Tyr Phe Ala Val Ala Leu Leu Gly Gly Gly Pro Leu
 130 135 140
 aat ggg atc ctg tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481
 Asn Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160
 atc tca tca gct cag ggg aag tat aag gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 cac ctc tca gtt gtc tcc tta ttt tat ggt aca tgc tta ggg gtg tac 577
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Cys Leu Gly Val Tyr
 180 185 190
 ctt agt tct gct gca acc cac aat tca cac aca ggt gct gca gcc tca 625
 Leu Ser Ser Ala Ala Thr His Asn Ser His Thr Gly Ala Ala Ala Ser
 195 200 205
 gtg atg tac act gtg gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro

215

38

[illegible]

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 46
<211> 649
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO19; Accession DDBJ/EMBL/GenBank = AF127846

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 46
c ttt gtg gac atc tgt ttc atc tcc acc aca gtc ccc aag atg cta gtg 49
Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act 97
Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20 25 30

cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg 145
Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
35 40 45

gct gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac 193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca 241
Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

tct tgg ttc atc att ttc tgg ttc tcg ctg gtt cat gtt cta ctg atg 289
Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met
85 90 95

aag agg ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt 337
Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
100 105 110

gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat 385
Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
115 120 125

aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta 433
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
130 135 140

gct ggg atc ctc ttc tcc tac tct cag att gtc tcc tcc tta atg aga 481
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
145 150 155 160

acg tcc tcc acc aag ggc aag tac aaa gcc ttt tcc acc tgt gga tct 529
Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

cac ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat 577
His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr

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180
185
190
ctg agt tct gct gtg acc cat tct tcc cag agc agc tcc atg gcc tca 625
Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
195 200 205

gtg atg tac gcc atg gtc acc ccc 649
Val Met Tyr Ala Met Val Thr Pro
210 215

<210> 47
<211> 216
<212> PRT
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO19; Accession DDBJ/EMBL/GenBank = AF127846

<400> 47
Phe Val Asp Ile Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20 25 30

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Val Leu Leu Met
85 90 95

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
145 150 155 160

Thr Ser Ser Thr Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

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His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
195 200 205

Val Met Tyr Ala Met Val Thr Pro
210 215

<210> 48
<211> 649
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO2; Accession DDBJ/EMBL/GenBank = AF127847

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 48
c ttt gta gac atc tgt gtt acc tcc acc aca gtc cca aag aca ctg tca 49
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
1 5 10 15

aac atc cgg aca cag agc aaa gtc atc acc tat gca ggt tgc atc acc 97
Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
20 25 30

cag atg tac ttt ttt ata ctc ttt gta gtg ttg gac agc tta ctc ctg 145
Gln Met Tyr Phe Phe Ile Leu Phe Val Val Leu Asp Ser Leu Leu Leu
35 40 45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac aca gtc att atg aac tcc tgg ctc tgt gga ctg ctg gtt ctg gtg 241
Tyr Thr Val Ile Met Asn Ser Trp Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80

tcc tgg atc gtg agc atc cta tgt tct ccg tta caa agc ata atg gca 289
Ser Trp Ile Val Ser Ile Leu Cys Ser Pro Leu Gln Ser Ile Met Ala
85 90 95

ttg cag ctg tcc ttc tgt aca gaa ttg aaa atc cct cat ttt ttc tgt 337
Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His Phe Phe Cys
100 105 110

gaa ctt aat cag gtc gtc cac ctt gcc tgt tct gac act ttt att aaa 385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Ile Lys
115 120 125

gac atg atg atg aat ttt aca agt gtg ctg ttg ggt ggg gga tgc ctc 433
Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu
130 135 140

gct gga ata ttt tac tct tac ttt aag ata ctt tgt tgc ata tgt tca 481
Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser

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145              150              155              160
atc tca cca gct cag ggg atg aat aaa gca ctt tcc acc tgt gca tct      529
Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser
              165              170              175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc gta ggt gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr
              180              185              190

ctt agt tct gct gca acc cat aac tca ctc tca aat gct gca gcc tca      625
Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser
              195              200              205

gtg atg tac acc gtg gtc acc tcc      649
Val Met Tyr Thr Val Val Thr Ser
              210              215

<210> 49
<211> 216
<212> PRT
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO2; Accession DDBJ/EMBL/GenBank = AF127847

<400> 49
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Val Pro Lys Thr Leu Ser
1              5              10              15

Asn Ile Arg Thr Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
              20              25              30

Gln Met Tyr Phe Phe Ile Leu Phe Val Val Leu Asp Ser Leu Leu Leu
              35              40              45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
              50              55              60

Tyr Thr Val Ile Met Asn Ser Trp Leu Cys Gly Leu Leu Val Leu Val
65              70              75              80

Ser Trp Ile Val Ser Ile Leu Cys Ser Pro Leu Gln Ser Ile Met Ala
              85              90              95

Leu Gln Leu Ser Phe Cys Thr Glu Leu Lys Ile Pro His Phe Phe Cys
              100              105              110

Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Ile Lys
              115              120              125

Asp Met Met Met Asn Phe Thr Ser Val Leu Leu Gly Gly Gly Cys Leu
              130              135              140

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Ala Gly Ile Phe Tyr Ser Tyr Phe Lys Ile Leu Cys Cys Ile Cys Ser
145 150 155 160

Ile Ser Pro Ala Gln Gly Met Asn Lys Ala Leu Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Val Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Asn Ala Ala Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Ser
210 215

<210> 50
<211> 649
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO3; Accession DDBJ/EMBL/GenBank = AF127848

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 50
c ttt gtg gac acc tct ttc atc tcc acc aca gtc ccc aag atg cta gtg 49
Phe Val Asp Thr Ser Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aac atc cag gca cgg atc aaa gac atc tcc tac atg ggg tgc ctc act 97
Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20 25 30

cag gtg tat ttt tta atg atg ttt gct gga atg gat act ttc cta ctg 145
Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
35 40 45

gcc gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc ctg cac 193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac acg gtc atc atg aac ccc tgc ctc tgt ggc ctc ctg gtt ctg gca 241
Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

tct tgg ttc atc att ttc tgg ttc tcc ctg gtt cat att cta ctg atg 289
Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
85 90 95

aag aag ttg acc ttc tcc aca ggc act gag att ccg cat ttc ttc tgt 337
Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
100 105 110

gaa ccg gct cag gtc ctc aag gtg gcc tgc tct aac acc ctc ctc aat 385
Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn


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115          120          125
aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta      433
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
130          135          140

gct ggg atc ctc ttc tcc tac tct cag att gtc tcc tcc tta atg aga      481
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
145          150          155

acg tcc tcc acc gag ggc aag tac aaa gcc ttt tcc acg ctg tgg atc      529
Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
165          170          175

tcc ctc tgt gtg gtc tcc ttg ttc tat gga aca gga ctt ggg gtc tat      577
Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180          185          190

ctg agt tct gct gtg acc cac tct tcc cag agc agc tcc atg gcc tca      625
Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
195          200          205

gtg atg tac gcc gtg gtc acc ccc      649
Val Met Tyr Ala Val Val Thr Pro
210          215

<210> 51
<211> 216
<212> PRT
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO3; Accession DDBJ/EMBL/GenBank = AF127848

<400> 51
Phe Val Asp Thr Ser Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1          5          10          15

Asn Ile Gln Ala Arg Ile Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20          25          30

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
35          40          45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50          55          60

Tyr Thr Val Ile Met Asn Pro Cys Leu Cys Gly Leu Leu Val Leu Ala
65          70          75          80

Ser Trp Phe Ile Ile Phe Trp Phe Ser Leu Val His Ile Leu Leu Met
85          90          95

Lys Lys Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
100          105          110

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Glu Pro Ala Gln Val Leu Lys Val Ala Cys Ser Asn Thr Leu Leu Asn
115 120 125

Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
130 135 140

Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
145 150 155 160

Thr Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Leu Trp Ile
165 170 175

Ser Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
195 200 205

Val Met Tyr Ala Val Val Thr Pro
210 215

<210> 52
<211> 650
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 9593; gene = GGO4; pseudogene; Accession DDBJ/EMBL/GenBank = AF127849

<400> 52
cttggctgag attggtttca tctcggtcgc ggttcccaag atgatcgtgg acatgcagtc 60
acatagcaga gtcattctct atgcggggcgc cctgacacag atgtctttct ttgtcctttt 120
tgcatgtatg gatgacatgc tccggactct gatggcctat gaccgatttg tggccatctg 180
tcaccccttg cactaccacg tcatcatgaa tcttcacctc tgtgtcttct tagtttttgt 240
gccttttttc cttagcctgt tggattccca gctgcacagc tggattgtgt tacaattcac 300
ttgcttcaag aatgtggaaa tatctaattt tttatgtgat ccatctcaac ttctcaaact 360
tgactgttct gaacagtgtc atcaatagca tattcacata tttagatagt actatgtttg 420
gtttccttcc catttcaggg atccttttgt ctactataa aattgtcccc tccattctaa 480
gaattccatc gtcagatggg aagtataaag ccctctccac ctgtggctct cacctgtcag 540
ttgtttgctt attttatgga ataggcattg gcgtgtacct gacttcagct gtgtcaccac 600
caccaggaa tgggtgtggtg gcatcagtga tctacgcggt ggtaaccccc 650

<210> 53
<211> 650
<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(650)

<223> Taxon = 9593; gene = GGO70; pseudogene; Accession DDBJ/EMBL/GenBank = GenBank = AF127850

<400> 53

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cttgctgac atcggtttca cctccaccat ggtccccaag atgattgtgg acgtccaatc      60
tcacagcagg ttcattctct atgcaggctg cctgactcag atatctctct ttgccatttt      120
tgagggcatt gaagagagac atgctcctga gtgtgatggc ctatgaccgg tttgtagcca      180
tctgtcaccc tctatatcat tcagccatca tgaaccctgt tttctgtggc ttccctagatt      240
tgctgtcttt tttttctttc tttttctcag tcttttagat ggtcagctgc agaacttgat      300
tgctttacaa atgacctgct tcgaggatgt gggaattcct aatttcctct gtgacccttc      360
tcaactgccc catctcacat gttgtgacat cttcaccaat cacataatca tgtatttccc      420
tgctgccata tttgggttttc ttcccatctc ggggaccctt ctctcttacc atgtaattgt      480
ttcctccatt ctgagggttt catcatctat gggagggtga aagccttccc cacctgtgag      540
ttgtttgctg atattatgga acaggcttcg gagggtaact cagttcagat gtgttatctt      600
caacaagaaa ggctgcagtg gcctcagtg tgtacacggg ggtcacgccc      650

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<210> 54

<211> 649

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9593; gene = GGO71; Accession DDBJ/EMBL/GenBank = AF127851

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 54

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t ttt gct gac ctc tgt ttt acc tcc acg act gtc cca aag atg tta ctg      49
  Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Leu
    1             5             10             15

aat ata ctg aca cag aac aaa ttc ata aca tat gca ggc tgt ctc ggt      97
Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
    20             25             30

cag att ttt ttt ttc act tca ttt gga tgc ctg gac aat tta ctc ttg      145
Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu Leu
    35             40             45

act gtg atg gcc tat gac cgc ttc gtg gcc atc tgt cac ccc ctg cac      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
    50             55             60

tat acg gtc atc atg aac ccc cgg ctc tgt gga ctg ctg gtt ctg ggg      241
Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly

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65              70              75              80
tcc tgg tgc atc agt gtc atg ggt tcc ctg ctc gag acc ttg act gtt      289
Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
                        85              90              95

ttg agg ctg tcc ttc tgc acc aaa atg gaa att cca cac ttt ttt tgt      337
Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys
                        100              105              110

gat ctt ctt gaa gtc ctg aag ctc gcc tgt tct gac acc ttc att aat      385
Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
                        115              120              125

aac gtg gtg ata tac ttt gca act ggc gtc ctg ggt gtg att ccc ttc      433
Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe
                        130              135              140

act gga ata ttt ttc tct tac tat aaa att gtt ttc tct ata ctg agg      481
Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
145              150              155              160

att tcc tca gct ggg aga aag cac aaa gcg ttt tcc acc tgt ggt tcc      529
Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
                        165              170              175

cac ctc tca gtg gtc acc ttg ttc tat ggc acg ggc ttt ggg gtc tat      577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
                        180              185              190

ctc agt tct gca gcc aca cca tct tct agg aca agt ctg gcg gcc tca      625
Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Ala Ala Ser
                        195              200              205

gtg atg tac acc atg gtc acc ccc      649
Val Met Tyr Thr Met Val Thr Pro
                        210              215

<210> 55
<211> 216
<212> PRT
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9593; gene = GGO71; Accession DDBJ/EMBL/GenBank = AF127851

<400> 55
Phe Ala Asp Leu Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Leu
1              5              10              15

Asn Ile Leu Thr Gln Asn Lys Phe Ile Thr Tyr Ala Gly Cys Leu Gly
20              25              30

Gln Ile Phe Phe Phe Thr Ser Phe Gly Cys Leu Asp Asn Leu Leu Leu
35              40              45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50              55              60

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Tyr Thr Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Gly
65 70 75 80

Ser Trp Cys Ile Ser Val Met Gly Ser Leu Leu Glu Thr Leu Thr Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Lys Met Glu Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Leu Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Phe Ile Asn
115 120 125

Asn Val Val Ile Tyr Phe Ala Thr Gly Val Leu Gly Val Ile Pro Phe
130 135 140

Thr Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Val Phe Ser Ile Leu Arg
145 150 155 160

Ile Ser Ser Ala Gly Arg Lys His Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Phe Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Ala Ala Ser
195 200 205

Val Met Tyr Thr Met Val Thr Pro
210 215

<210> 56
<211> 649
<212> DNA
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 13515; gene = EFU35; Accession DDBJ/EMBL/GenBank = AF127852

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 56
c ctc act gac atc tgt tta agc aca gcc acc gtc cca aag atg ctg gca 49
Leu Thr Asp Ile Cys Leu Ser Thr Ala Thr Val Pro Lys Met Leu Ala
1 5 10 15

aac atc cga aca cgg agt cag agc atc acg tat gca gcc tgc ctc acc 97
Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr
20 25 30

cag atg tgc ttt gtt ctg ggt tct gct acg ttg gaa aat ttt ctc ctg 145
Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu

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      35              40              45
gca gta atg gct tat gac cgc tat gtg gcc atc tgt cat cct ctg aga      193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
      50              55              60

tac gcg gtc atc atg aac ctt cgt ctc tgt ggc ttc ttg atc ctt ttg      241
Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu
      65              70              75

tcc ctg tct att agc atc atg gac acc ctg ctc cac gat ctg atg gtc      289
Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val
      85              90              95

ttg cgg ctg tcc ttc tgc aca cac ctg gag ata ccc ctc ttc ttc tgc      337
Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys
      100             105             110

gag gtt gtg caa gtc atc aag ctt gcc tgt tct gat acc ctc atc aat      385
Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn
      115             120             125

aac ctc ttg ata tat ttt gca gct ggc gtg ttg gga ggt gtt cct ctg      433
Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu
      130             135             140

tct ggg atc att ttc tct tat act cag att gcc tcc tct gtt ttg aga      481
Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg
      145             150             155

atg gca tca gca agt gga aag tat aaa gct ttt tcc acc tgt ggc tct      529
Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
      165             170             175

cac ctc tcg gtt gtg tcc ttg ctc tac ggg aca ggt ttg ggg gtg tac      577
His Leu Ser Val Val Ser Leu Leu Tyr Gly Thr Gly Leu Gly Val Tyr
      180             185             190

atc agt tct gcg ttt atg cac tct ccc agg acg atg gca gtg gct tca      625
Ile Ser Ser Ala Phe Met His Ser Pro Arg Thr Met Ala Val Ala Ser
      195             200             205

atg atg tac acg gtg gtc act ccc                                     649
Met Met Tyr Thr Val Val Thr Pro
      210             215

<210> 57
<211> 216
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 13515; gene = EFU35; Accession DDBJ/EMBL/GenBank = AF127852

<400> 57
Leu Thr Asp Ile Cys Leu Ser Thr Ala Thr Val Pro Lys Met Leu Ala
1              5              10              15

Asn Ile Arg Thr Arg Ser Gln Ser Ile Thr Tyr Ala Ala Cys Leu Thr
20             25             30

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Gln Met Cys Phe Val Leu Gly Ser Ala Thr Leu Glu Asn Phe Leu Leu
35 40 45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Arg
50 55 60

Tyr Ala Val Ile Met Asn Leu Arg Leu Cys Gly Phe Leu Ile Leu Leu
65 70 75 80

Ser Leu Ser Ile Ser Ile Met Asp Thr Leu Leu His Asp Leu Met Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr His Leu Glu Ile Pro Leu Phe Phe Cys
100 105 110

Glu Val Val Gln Val Ile Lys Leu Ala Cys Ser Asp Thr Leu Ile Asn
115 120 125

Asn Leu Leu Ile Tyr Phe Ala Ala Gly Val Leu Gly Gly Val Pro Leu
130 135 140

Ser Gly Ile Ile Phe Ser Tyr Thr Gln Ile Ala Ser Ser Val Leu Arg
145 150 155 160

Met Ala Ser Ala Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Leu Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

Ile Ser Ser Ala Phe Met His Ser Pro Arg Thr Met Ala Val Ala Ser
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 58

<211> 645

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(645)

<223> Taxon = 13515; gene = EFU36; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127853

<400> 58

ctttgctgac gtctgtttca cctccaccac ggtgcccaag atgttagtga acatccaggc 60

gcacagcaag gccatcacat acaaaggctg cctcaccag atgtgttttt tcttgatttt 120

tggtgggcta gtttgctact gacgggtgatg gcctatgacc gggtcgtggc catctgtcac 180

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ccccgcgct acatggteat catgaacccc aggcctctgtg gtctttctgct tctcctttct 240
tggttgatct gcttgacgta ttctctgctg caaagtctga tggttttgag ggtgtccttc 300
tgccaagaaa tagaaatccc ccactacttc tgtgaacttg ctcagatcct cacgctcgcc 360
tgctctgaca ccctagttaa tgacgtcctg ctgtattttc tatctgctct gctcgggtgtt 420
attccctga ctgggatcct ttattcttat tccagaatta tctcctccat aatgtgcatt 480
tcctctgctg gagggaagta caaagccttt tccacctgtg ggtctcacct ctccgtcgtc 540
tccttggtct acggtacagg ccttggggtc tacctaactt ctgaaacagc ccagccctcc 600
agaaggggtt caatagcctc ggtgatgtac accatgggtca ccccc 645

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<210> 59
<211> 647
<212> DNA
<213> Eulemur fulvus

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<220>
<221> misc_feature
<222> (1)..(647)
<223> Taxon = 13515; gene = EFU37; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127854

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<400> 59
ctttgttgac atctgtttca cctccaccac catccccaag atgactgtgg acatcctaac 60
tcacagcaga gtcattctct ctgggggctg tctgaccag atgtctcttg ctctgctttt 120
tgtttggtgt gatgatatgc ttctgaccgt gtcggcctgt gacctgtttg tggccatctg 180
ccacccctg cactacacgg tcattcatgaa cccccacttc tgtggcctcc tggttctgat 240
atcttggttc atcatgtccc tggttgtcct ggttcacctc ctactgataa ggaggctgac 300
attccccagg gccacagaaa tcccacatta cttctgtgaa ctgggtcaaa ttctcaaagt 360
ggcccaactct gacagcttca tcaataacat ctcttgttac ttgtcggctg tgttgctggg 420
tgtgtttccc atcacaggga tcctctactc ctactctaaa attgtctcct ccgtaatgag 480
gatgtcgtcc actgcaggca agaagaaagc attttccacc tgtgggtctc atttgtgtgg 540
tctgcttggt ctatggaaca gggcttgggg tctacctcag ctctgctgtg accccttctt 600
cccagagcag cagcattgcc tcagtgatgt actcgggtgg caccccc 647

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<210> 60
<211> 652
<212> DNA
<213> Eulemur rubriventer

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<220>
<221> misc_feature
<222> (1)..(652)
<223> Taxon = 34829; gene = ERU38; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127855

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<400> 60
ctttgttgac atctgtttca cctccaccac catccccaag atgctgggtga acattgacac 60

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acacagcaaa gacatctcct acgtgggatg cctcactcag atgtattttt tcatggtgtt      120
tggtggactg gacaacttcc tctgaccgt gatggcctgt gaccggtttg tggccatctg      180
tcacccctg cactatgcag tacagtcac atgaaccccc gcttctgtgc cctcctggtt      240
ctgatgtctt gggtcatcat gtccctggat gcctgggttc atgttctact tatactgagg      300
ctgacctttt ccttagaaac tgaaatccca catttcttct gtgacctggc tcagatgttc      360
gagggtggcc gctctgacac ctttatcaat aacatctgct tgtacttggt ggctgtgttg      420
ctgtatgttt cctgtcacgg ggatcctcta ccctactctt aaaattgtct cctccttaat      480
gaggatgtcc tccactgcag gcaagaagaa agcattttcc acctgtgggt ctcacctctc      540
tgtggtcttc ttgttctatg gaacaggact tggggtctac ctaagttctg ctgtgacccc      600
ttcttcccag agcagcgcca ttgcctcagt gatgtacaca gtagtcaccc cc              652

<210> 61
<211> 648
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 34829; gene = ERU39; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127856

<400> 61
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gagcaaagtc atatcctaca caggctgcat caccagatg gactttttct tgctctttgt      120
aggactggac aacttctctc tgaccgtgat ggctgtgac cggtttgtgg ccatctgtca      180
ccccctgcac tatgcagtac agtcatcatg aaccccaggc tctgtgcatt tcttgttctg      240
gtgttctgga tctgagtggt cctgaattcc ttgttacaaa gcttaatggg gttgcagata      300
accttctgta cagacttggg aatccccccac tttttctgtg aacttaatca gataatccac      360
cttgctgtgt tggacacctt tottaatgac atggatgatg atttggcagt gatgctgctg      420
gggtgggggg gccttactgg gatcctttac tcttactcta agatagtttc ctccgtacgt      480
gcaatctcct cggtcaggg gaagtataaa gcattttcca cctgtgcac tcacctctcg      540
gtcgtctcct tattttattg tacatgccta ggggtgtacc tcagttctgc tacacacaac      600
tcacactcca ggcgaacagc ctgggtgatg tacacgggtg tcaactccc              648

<210> 62
<211> 649
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 34829; gene = ERU40; Accession DDBJ/EMBL/GenBank = AF127857

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<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 34829; gene = ERU40; Accession DDBJ/EMBL/GenBank = AF127857

<400> 63

Leu Ser Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
1 5 10 15

Asn Leu His Ala His Ser Lys Asp Ile Ser Tyr Arg Glu Cys Leu Thr
20 25 30

Gln Val Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Met Val Ile Met Asn Pro Arg Phe Cys Ala Leu Leu Val Leu Met
65 70 75 80

Ser Trp Phe Ile Met Ser Leu Val Ala Leu Val His Val Leu Leu Ile
85 90 95

Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Ser Cys
100 105 110

Glu Val Ala Gln Ile Leu Lys Val Ala Arg Ser Asp Thr Phe Phe Asn
115 120 125

Asn Ile Cys Leu Tyr Leu Ser Ala Val Leu Leu Gly Val Phe Pro Val
130 135 140

Met Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg
145 150 155 160

Met Ser Ser Thr Ser Ala Lys Asn Lys Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Cys Val Val Ser Leu Phe Tyr Gly Thr Ala Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ala Ile Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 64

<211> 648

<212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(648)
 <223> Taxon = 13515; gene = EFU56; pseudogene; Accession DDBJ/EMBL/GenBank = AF127858

<400> 64
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 acacagcaaa gccatatcct acgcaggctg tgtcaccag atgcactttt gcataacggt 120
 tgcagagtag gcattcttct cctgactgtg atggcctatg actggtttgg ggccatctgt 180
 caccctctgc actatgtgct catcatgaac cccaggctct gtgcactgct tgttctggtg 240
 tcttggatca tgagtgtcct gaattccttg ttgcaaagct taatggtgtt gccactgccc 300
 ttctgtgcag agttggaaat cccccagttt ttctgtgaac ttaatcagat aatcctcctt 360
 gcctgttctg acacctttct taatgacgtg gtgatgtatt tggcagctat gctactgggt 420
 gaggggtgcc ttactgggat cctttactct tactctaaga tagtttcctc cgtacgtgca 480
 atctcctcgg ctcaggggaa gtataaagca ttttccacct gtgcattctca cctctcggtc 540
 gtctccttat ttactgcac aagcctcggg gtgtacctcg gctctgctgc tacacacaac 600
 tcacactcca ggcgaacagc ctcggtgatg tacacggtgg tcactccc 648

<210> 65
 <211> 643
 <212> DNA
 <213> Eulemur fulvus

<220>
 <221> misc_feature
 <222> (1)..(643)
 <223> Taxon = 13515; gene = EFU57; Accession DDBJ/EMBL/ GenBank = AF127859

<220>
 <221> CDS
 <222> (2)..(643)
 <223> Product = olfactory receptor

<400> 65
 c ttt gca gac atc tgt ttt gtg tcc acc act gtc cca gag atg ctg aat 49
 Phe Ala Asp Ile Cys Phe Val Ser Thr Thr Val Pro Glu Met Leu Asn
 1 5 10 15
 gtg cag aca tgg agc aaa gtc ata tct tac aca ggc tgc atc acc cag 97
 Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln
 20 25 30
 atg gac ttt ttc ttg ctc ttt gta gga ctg gac aac ttc ctc ctg acc 145
 Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr
 35 40 45
 gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cgc tat 193
 Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
 50 55 60
 gca gtc atc atg aac ccc agg ctc tgt gta ttt ctt gtt ctg gtg tcc 241

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Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser
65              70              75              80

tgg atc ctg agt gtc ctg aat tcc ttg tca caa agc tta atg gtg ttg      289
Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu
      85              90              95

cgg cta acc ttc tgt aca gac ttg gaa atc ccc cac ttt ttc tgt gaa      337
Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu
      100             105             110

ctt aat cag ata atc cac ctt gcc tgt tcg gac acc ttt ctt aat gac      385
Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp
      115             120             125

gtg gtg atg tat ttg gca gtg atg ctg ctg ggt ggg gga tgc ctt act      433
Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Gly Cys Leu Thr
      130             135             140

ggg atc ctt tac tct tac tct aag ata gtt tcc tcc gta cgt gca atc      481
Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile
      145             150             155             160

tcc tcg gct cag ggg aag tgt aaa gca ttt tcc acc tgt gca tct cac      529
Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His
      165             170             175

ctc ttg gtc gtc tcc tta ttt tat tgt aca tgc cta ggg gtg tac ttg      577
Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu
      180             185             190

agt tct gct aca cac aac tca cac tcc agc gca aca gcc tcg gtg atg      625
Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met
      195             200             205

tac acg gtg gtc act ccc      643
Tyr Thr Val Val Thr Pro
      210

<210> 66
<211> 214
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 13515; gene = EFU57; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127859

<400> 66
Phe Ala Asp Ile Cys Phe Val Ser Thr Thr Val Pro Glu Met Leu Asn
1              5              10              15

Val Gln Thr Trp Ser Lys Val Ile Ser Tyr Thr Gly Cys Ile Thr Gln
      20              25              30

Met Asp Phe Phe Leu Leu Phe Val Gly Leu Asp Asn Phe Leu Leu Thr
      35              40              45

Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg Tyr
      50              55              60

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Ala Val Ile Met Asn Pro Arg Leu Cys Val Phe Leu Val Leu Val Ser
65 70 75 80

Trp Ile Leu Ser Val Leu Asn Ser Leu Ser Gln Ser Leu Met Val Leu
85 90 95

Arg Leu Thr Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys Glu
100 105 110

Leu Asn Gln Ile Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn Asp
115 120 125

Val Val Met Tyr Leu Ala Val Met Leu Leu Gly Gly Gly Cys Leu Thr
130 135 140

Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala Ile
145 150 155 160

Ser Ser Ala Gln Gly Lys Cys Lys Ala Phe Ser Thr Cys Ala Ser His
165 170 175

Leu Leu Val Val Ser Leu Phe Tyr Cys Thr Cys Leu Gly Val Tyr Leu
180 185 190

Ser Ser Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser Val Met
195 200 205

Tyr Thr Val Val Thr Pro
210

<210> 67
<211> 644
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(644)
<223> Taxon = 34829; gene = ERU66; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127860

<400> 67
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acagagcaaa tccatcacccg gtgccggctg cctcacacag atgtactgtt tcatggcttt 120
tggacttctg gacaatctga tgctgatggt catggcttat gaccactttg tggccatctg 180
tcaccctctg cactacacag tcatcatgaa cccagtgtc tgtgtccagg tgcttgtcca 240
caccgggctt gtcagcatcc tgggggcctt cctcggagag tgaccgtgtt gcggcttctt 300
ttggtgcagt cactgaaatc ccacactatt tctgtgagct cctgaggct ctccagctct 360

atc ccc tct gca gcc ggg aag tgg aag gcc ttc tcc acc tgt ggc tcc 529
 ile pro ser ala ala gly lys trp lys ala phe ser thr cys gly ser
 165 170 175

cac ctc act gtg gtg gtc ctg ttc tat ggc agt gtc atc tat gtg tat 577
 his leu thr val val val leu phe tyr gly ser val ile tyr val tyr
 180 185 190

ttc agg ccc ctg tcc atg tac tca gtg atg aag gac cgg gta gcc aca 625
 phe arg pro leu ser met tyr ser val met lys asp arg val ala thr
 195 200 205

gtt atg tac acg gta gtg aca cct 649
 val met tyr thr val val thr pro
 210 215

<210> 69
 <211> 216
 <212> PRT
 <213> Eulemur rubriventer

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 34829; gene = ERU67; Accession DDBJ/EMBL/GenBank = AF127861

<400> 69
 phe met asp ile cys phe thr thr val ile val pro lys met leu val
 1 5 10 15

asn phe leu ser glu thr lys ala ile ser tyr val gly cys leu val
 20 25 30

gln met tyr phe phe met ala leu ala asn thr asp ser tyr leu leu
 35 40 45

ala ser met ala ile asp arg leu val ala ile cys lys pro phe his
 50 55 60

tyr asp val val met ser pro arg arg cys leu leu met leu leu gly
 65 70 75 80

ser cys thr ile ser his leu his ser leu phe arg val leu leu met
 85 90 95

ser arg leu ser phe cys ala ser his ile ile lys his phe phe cys
 100 105 110

asp thr gln pro val leu lys leu ser cys ser asp thr ser ser ser
 115 120 125

gln ile val val met thr glu thr leu ala val ile val thr pro phe
 130 135 140

leu cys ile ile phe ser tyr leu arg ile ile ile thr val leu ala

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	3500	1500	1000	6000
Health	0.5	0.5	0	1
Smoking	0.2	0.4	0	1
Alcohol	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.4	0.5	0	1
Sleep	0.5	0.5	0	1
Diet	0.5	0.5	0	1
Work	0.5	0.5	0	1
Family	0.5	0.5	0	1
Friends	0.5	0.5	0	1
Hobbies	0.5	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.5	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.5	0.5	0	1
Fishing	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Cooking	0.5	0.5	0	1
Cleaning	0.5	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.5	0.5	0	1
Traveling	0.5	0.5	0	1
Working	0.5	0.5	0	1
Studying	0.5	0.5	0	1
Playing	0.5	0.5	0	1
Watching	0.5	0.5	0	1
Eating	0.5	0.5	0	1
Drinking	0.5	0.5	0	1
Smoking	0.5	0.5	0	1
Alcohol	0.5	0.5	0	1
Exercise	0.5	0.5	0	1
Stress	0.5	0.5	0	1
Sleep	0.5	0.5	0	1
Diet	0.5	0.5	0	1
Work	0.5	0.5	0	1
Family	0.5	0.5	0	1
Friends	0.5	0.5	0	1
Hobbies	0.5	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.5	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.5	0.5	0	1
Fishing	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Cooking	0.5	0.5	0	1
Cleaning	0.5	0.5	0	1
Shopping	0.5	0.5	0	1
Driving	0.5	0.5	0	1
Traveling	0.5	0.5	0	1
Working	0.5	0.5	0	1
Studying	0.5	0.5	0	1
Playing	0.5	0.5	0	1
Watching	0.5	0.5	0	1
Eating	0.5	0.5	0	1
Drinking	0.5	0.5	0	1
Smoking	0.5	0.5	0	1
Alcohol	0.5	0.5	0	1
Exercise	0.5	0.5	0	1
Stress	0.5	0.5	0	1
Sleep	0.5	0.5	0	1
Diet	0.5	0.5	0	1
Work	0.5	0.5	0	1
Family	0.5	0.5	0	1
Friends	0.5	0.5	0	1
Hobbies	0.5	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.5	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.5	0.5	0	1
Fishing	0.5	0.5	0	1
Reading	0.5	0.5	0	

60


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115              120              125

Asp Met Val Met Tyr Phe Ser Ala Leu Leu Leu Gly Gly Gly Ser Leu
130              135              140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Val Arg Ala
145              150              155              160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165              170              175

His Leu Ala Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
180              185              190

Leu Ser Ser Ala Ala Thr His Asn Ser His Ser Ser Ala Thr Ala Ser
195              200              205

Val Met Tyr Thr Val Val Thr Pro
210              215

<210> 72
<211> 642
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(642)
<223> Taxon = 34829; gene = EFU84; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127863

<400> 72
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acacagcagt catatcctat gcaggctgtg tcaccagat gcacttttcc ataatctttg 120
cagagttaga catcttcctc ctgacggtga tggcctatga ccggtgtgtg gccatctgtc 180
acccctgca ctacacggcc atcatgaacc ccaggctctg tgaactgctg gttctggctt 240
cctggatcat aagtggcccg aattccttgt taciaagtgt aaagggtgctg tggctgtcct 300
tctgtacaaa cttggaaatc cgtcactttt tctgtgaact tagatactac atcttgctg 360
ttgtgacacc tctgttcattg acgtggtgat acatattgca gctgtggtgc tggctgtttt 420
tcctcttget gggatccttt actcttactc tcagatagtt tcctccacac gtgcactctc 480
ctcagctcag gcgaagtgtg aagcattttc cacctgtgca gctcacctcg cggttgtctc 540
tctattttac tgcacaagcc tcgggggtgta cttgagctct gctgctacac acaaccaca 600
ctccagcgca acagcctcgg tgatgtacat ggtgggtcact cc 642

<210> 73
<211> 652
<212> DNA
<213> Eulemur fulvus

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<220>
 <221> misc_feature
 <222> (1)..(652)
 <223> Taxon = 13515; gene = EFU86; pseudogene; Accession DDBJ/EMBL/GenBank = AF127864

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 acagagcaaa gtcatactct acgcaggctg cgtcaccag atggactttt tcatactctt 120
 tgcagggttg gatattctta tgctgatcat gatggcctat gaccgggttg gggccatctg 180
 tcaccactg cagtacacgg tcatacatgaa cccagggctc tgtgggctgc tggttgtggt 240
 gccctggatc ttgagtgacc tgaattcctt gttacaaagc ttaatggtgt tgtcactgtc 300
 cttttgtaga cacttggaag tcttcacttt ttctgtgaac ttaatcaggt tgtccacctt 360
 gcctgttctg aaaccttctt taatgacatg gtgatgtatc tgatatctgt ggtgctgggt 420
 ggtggttccc tggctgggac tctttattct ttcttactgc agaatagttt gctccatacg 480
 tgcaacgtcc tcagctcagg ggaagtataa agcatttccc acctgtgcat ctcacctctc 540
 agttgtctcc ttatcttctt gcacaatcct aggggtgtac ctcagctctg ctgctaccca 600
 gaattcgtgc tccagtgcag tagccttggg ggtgtacacg gtggtcactc cc 652

<210> 74
 <211> 649
 <212> DNA
 <213> Eulemur fulvus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 13515; gene = EFU87; Accession DDBJ/EMBL/GenBank = AF127865

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 74
 c ttt gtt gac atc tgt ttc acc tcc acc acc atc ccc aag atg ctg gtg 49
 Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 aac att gaa aca cac agc aaa gac atc tcc tac atg gga tgc ctc act 97
 Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
 20 25 30
 cag atg tat ttt ttc atg att ttt gct gga ctg gat aat ttc ctc ctg 145
 Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
 35 40 45
 act gtg atg gcc tat gac cgg ttt gtg gcc atc tgc cac ccc tta cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac acg gtc atc atg agt ccc cgc ttc tgt gcc ctc ctg gtt ctc ata 241
 Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile
 65 70 75 80

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tct tgg ttc atc atg acc ctg gtt gcc ctg gtt cat gta cta ctg ata      289
Ser Trp Phe Ile Met Thr Leu Val Ala Leu Val His Val Leu Leu Ile
                        85                        90                        95

ttg agg ctg acc ttc tct tta gaa act gaa atc cca cat ttc ttc tgt      337
Leu Arg Leu Thr Phe Ser Leu Glu Thr Glu Ile Pro His Phe Phe Cys
                        100                        105                        110

gac ctg gct cag att ctc gag gtg gcc cac tct gat acc ctc atc aat      385
Asp Leu Ala Gln Ile Leu Glu Val Ala His Ser Asp Thr Leu Ile Asn
                        115                        120                        125

aac atc tgc atg tac ttg tgc act gtg ttg ctg ggc gtg ttt cct gtc      433
Asn Ile Cys Met Tyr Leu Ser Thr Val Leu Leu Gly Val Phe Pro Val
                        130                        135                        140

acg ggg atc ctc ttc tcc tac tct aaa att gtc tcc tcc tta atg agg      481
Thr Gly Ile Leu Phe Ser Tyr Ser Lys Ile Val Ser Ser Leu Met Arg
145                        150                        155                        160

atg tcc tcc act gca ggc aag aag aaa gca ttt tcc acc tgt ggg tct      529
Met Ser Ser Thr Ala Gly Lys Lys Lys Ala Phe Ser Thr Cys Gly Ser
                        165                        170                        175

cac ctc tct gtg gtc tgc ttg ttc tgc gga aca gga gtt ggg gtc tat      577
His Leu Ser Val Val Cys Leu Phe Cys Gly Thr Gly Val Gly Val Tyr
                        180                        185                        190

ctc agt tct gct gtg acc cct tct tcc cag agc agc agc att gcc tca      625
Leu Ser Ser Ala Val Thr Pro Ser Ser Gln Ser Ser Ser Ile Ala Ser
                        195                        200                        205

gtg atg ttc acg gtg gtc acc ccc                                     649
Val Met Phe Thr Val Val Thr Pro
210                        215

<210> 75
<211> 216
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 13515; gene = EFU87; Accession DDBJ/EMBL/GenBank = AF127865

<400> 75
Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Ile Pro Lys Met Leu Val
1                        5                        10                        15

Asn Ile Glu Thr His Ser Lys Asp Ile Ser Tyr Met Gly Cys Leu Thr
20                        25                        30

Gln Met Tyr Phe Phe Met Ile Phe Ala Gly Leu Asp Asn Phe Leu Leu
35                        40                        45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50                        55                        60

Tyr Thr Val Ile Met Ser Pro Arg Phe Cys Ala Leu Leu Val Leu Ile

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gtcctccacc gagggcaagt gcaaagcctt ttccacctgt gggctcacc tctgtgtggg 540
 ctccttggtc tatggaacag gacttggggg ctatctcagt tctgtgtgga cccattcttc 600
 ccagagcagc tccatggcct cagtgatgta caccatgggc accccc 646

<210> 77
 <211> 649
 <212> DNA
 <213> *Macaca sylvanus*

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY12; Accession DDBJ/EMBL/GenBank = AF127867

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 77
 c ttc gta gac gtc tgt ttt gtg tcc acc act gtc ccg aag atg ctg gtg 49
 Phe Val Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag aca cag aac aaa gtc atc acc tat gca ggc tgc atc agc 97
 Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Ser
 20 25 30
 cag atg tgc ttt ttc ata ttc ttt gca gga ttg gac atc ttt atg ctg 145
 Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
 35 40 45
 acc gtg atg gcc tac gac agg ttt gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac acg gtc acc atg aac ccc agg ctg tgt gga ctg ctg gtt ctg gcg 241
 Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80
 tcc tgg atc atg agt gcc ctg aat tct tca ttg caa agc tta atg gta 289
 Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val
 85 90 95
 ttg cac ctt tcc ttc tgt gca gac ttg gaa att ccc cac ttt ttc tgt 337
 Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110
 gaa ctt aat cag gtc atc cac ctt acc tgt tct gac act ttt ctt aat 385
 Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn
 115 120 125
 gac atg gtg atg tat ttg tca gct gtg ctg ctg ggt ggg gga tgt ctg 433
 Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu
 130 135 140
 att ggg atc ctt tac tct tac tct aag atc gtc tcc tct ata cat gca 481
 Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala
 145 150 155 160
 atc tca tca gtt cag ggg aag tac aag gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

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                165                170                175
cac ctc tcg gtt gtc tcc tta ttt tat tgt aca atc cta ggt gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr
                180                185                190

ctt agt tct gct gca acc cac agc tca cac gca agt gct gca gtc tcg      625
Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
                195                200                205

gtg atg tac act gtg gtt acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
                210                215

<210> 78
<211> 216
<212> PRT
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY12; Accession DDBJ/EMBL/GenBank = AF127867

<400> 78
Phe Val Asp Val Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1                5                10                15

Asn Ile Gln Thr Gln Asn Lys Val Ile Thr Tyr Ala Gly Cys Ile Ser
                20                25                30

Gln Met Cys Phe Phe Ile Phe Phe Ala Gly Leu Asp Ile Phe Met Leu
                35                40                45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50                55                60

Tyr Thr Val Thr Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65                70                75                80

Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Met Val
                85                90                95

Leu His Leu Ser Phe Cys Ala Asp Leu Glu Ile Pro His Phe Phe Cys
                100                105                110

Glu Leu Asn Gln Val Ile His Leu Thr Cys Ser Asp Thr Phe Leu Asn
115                120                125

Asp Met Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Cys Leu
130                135                140

Ile Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile His Ala
145                150                155                160

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Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ile Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr His Ser Ser His Ala Ser Ala Ala Val Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 79
<211> 649
<212> DNA
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 79
c ttg gct gac atc ggt ttc acc tcc acc aca gtc ccc aag atg ctg gtg 49
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15
aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc 97
Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
20 25 30
cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc 145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
35 40 45
acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac 193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
50 55 60
tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg 241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65 70 75 80
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg 289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95
ctg cag ttg tcc ttt tgc acc agt tgg gtc att cag cac ttt tac tgc 337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
100 105 110
gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat 385
Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
115 120 125
tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc 433
Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe

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130          135          140
tca gga atc ctt ttc tcc tac acc caa att gtc tcc tcc atc ctg aga      481
Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
145          150          155          160

atc tca tcc aca gat ggg aaa cac aaa gcc ttt tct aac tgc gga tct      529
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser
165          170          175

cat ctg tct gtg gtt ttt tta ttc tat ggg aca ggc ctt ggt gtg tat      577
His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180          185          190

ctt agt tcc aat gca tcg tcc tct tcc tgg cgg ggc atg gtg gcc tcg      625
Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser
195          200          205

gtc atg tac act gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
210          215

<210> 80
<211> 216
<212> PRT
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY16; Accession DDBJ/EMBL/GenBank = AF127868

<400> 80
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1          5          10          15

Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
20          25          30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
35          40          45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
50          55          60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65          70          75          80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85          90          95

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
100          105          110

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
115          120          125

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Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
 130 135 140

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Asn Cys Gly Ser
 165 170 175

His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 81
 <211> 647
 <212> DNA
 <213> *Macaca sylvanus*
 <220>
 <221> misc_feature
 <222> (1)..(647)
 <223> Taxon = 9546; gene = MSY2; pseudogene; Accession DDBJ/EMBL/GenBank = AF127869

<400> 81
 cttcgtagac gtctgttttg tgtccaccac tgtcccgaag atgctggtga acatccagac 60
 acagaacaaa gtcacacact atgcaggctg catcagccag atgtgctttt tcatattott 120
 tgcaggattg gacaccttta tgctgaccgt gatggcctac gacaggtttg tggccatctg 180
 tcaccctctg cactacacgg tcaccatgaa cccaggctc tgtggactgc tggttctggc 240
 gtcctgatca tgagtgcctt gaattcttca ttgcaaagct taatgggtatt gcacctttcc 300
 ttctgtgcag acttggaaat tcccactttt ttctgtgaac ttaatcaggt catccacott 360
 acctgttctg acacttttct taatgacatg gtgatgtatt tgtcagctgt gctgctgggt 420
 gggggatgtc tcattgggat cctttactct tactctaaga tcgtctctc tatacttgca 480
 atctcatcag ttcaggggaa gtacaaggca tttccacct gtgcatctca cctctcggtt 540
 gtctccttat ttattgtaca atoctagggt tgtaccttag ttctgctgca acccacagct 600
 cacacgcaag tgctgcagtc tcggtgatgt acactgtggt taccccc 647

<210> 82
 <211> 649
 <212> DNA
 <213> *Macaca sylvanus*

<220>
 <221> misc_feature

<222> (1)..(649)
 <223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

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<400> 82
c ttc ata gac atc tgt ttt gtg tcc acc act gtc ccg aag atg atg gtg      49
  Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Met Val
    1             5             10             15

aac atc cag aca cag agc aga gtc atc acc tat gca ggc tgc atc acc      97
Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
      20             25             30

cag atg tgc ttt ttc ata ttc ttt gtg gga ctg gat atc ttt atg ctg      145
Gln Met Cys Phe Phe Ile Phe Phe Val Gly Leu Asp Ile Phe Met Leu
      35             40             45

acc gtg atg gcc ttt gac cgg ttt gtg gcc atc tgt cac ccc ctg cac      193
Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50             55             60

tac acg gtc acc atg aac ccc agg ctc agt ggg ctg ctg gtt ctg gcg      241
Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala
      65             70             75             80

tcc tgg atc atg agt gcc ctg aat tcc tcg tta caa agc tta ata gtg      289
Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
      85             90             95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa att ccc cac ttt ttc tgt      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
      100            105            110

gaa ctt aat cag gtg gtc cac ctt gcc tgt tct gac acc ttt ctt aat      385
Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
      115            120            125

gac atg gtg atg tat ttg gca tct gca ctg ctg ggc tgt ggt ccc ctc      433
Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu
      130            135            140

tct ggg atc ctt tat tct tat tct aag atc gtt tcc tcc ata cgt gga      481
Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
      145            150            155            160

atc tca tca gct cag ggg aag tac agg gca ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser
      165            170            175

cac ctc tca gtt gtc tcc tta ttt tat ggt acg ctc cta gga gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
      180            185            190

ttt agt tct gct gca acc cgt aac tca cac tca agt gct gca gcc tcg      625
Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
      195            200            205

gtg atg tac acc gtg gtt acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
      210            215

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<210> 83
 <211> 216
 <212> PRT
 <213> *Macaca sylvanus*

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY4; Accession DDBJ/EMBL/GenBank = AF127870

<400> 83
 Phe Ile Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Met Val
 1 5 10 15

 Asn Ile Gln Thr Gln Ser Arg Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30

 Gln Met Cys Phe Phe Ile Phe Phe Val Gly Leu Asp Ile Phe Met Leu
 35 40 45

 Thr Val Met Ala Phe Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

 Tyr Thr Val Thr Met Asn Pro Arg Leu Ser Gly Leu Leu Val Leu Ala
 65 70 75 80

 Ser Trp Ile Met Ser Ala Leu Asn Ser Ser Leu Gln Ser Leu Ile Val
 85 90 95

 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

 Glu Leu Asn Gln Val Val His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125

 Asp Met Val Met Tyr Leu Ala Ser Ala Leu Leu Gly Cys Gly Pro Leu
 130 135 140

 Ser Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Gly
 145 150 155 160

 Ile Ser Ser Ala Gln Gly Lys Tyr Arg Ala Phe Ser Thr Cys Ala Ser
 165 170 175

 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190

 Phe Ser Ser Ala Ala Thr Arg Asn Ser His Ser Ser Ala Ala Ala Ser
 195 200 205

 Val Met Tyr Thr Val Val Thr Pro
 210 215

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<210> 84
<211> 646
<212> DNA
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 9546; gene = MSY6; Accession DDBJ/EMBL/GenBank = AF127871

<220>
<221> CDS
<222> (2)..(646)
<223> Product = olfactory receptor

<400> 84
c ttc act gac ctc ttc ttt gtc acc aac aca atc ccc aag atg ctg gtg      49
  Phe Thr Asp Leu Phe Phe Val Thr Asn Thr Ile Pro Lys Met Leu Val
    1             5             10             15

aac ctc cag tcc cag aac aaa gcc atc tcc tat gca ggg tgt ctg aca      97
Asn Leu Gln Ser Gln Asn Lys Ala Ile Ser Tyr Ala Gly Cys Leu Thr
          20             25             30

cag ctc tac ttc ctg gtc tcc ttg gtg gcc ctg gac aac ctc atc ctg      145
Gln Leu Tyr Phe Leu Val Ser Leu Val Ala Leu Asp Asn Leu Ile Leu
          35             40             45

gct gtg atg gcg tat gac cgc tat gtg gcc atc tgc tgc ccc ctc cac      193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Cys Pro Leu His
          50             55             60

tac acc aca gcc atg agc cct aag ctc tgt atc tta ctc ctt tcc ttg      241
Tyr Thr Thr Ala Met Ser Pro Lys Leu Cys Ile Leu Leu Leu Ser Leu
          65             70             75             80

tgt tgg gtc tta tct gtg ctc tat ggc ctc ata cac acc ttc ctc atg      289
Cys Trp Val Leu Ser Val Leu Tyr Gly Leu Ile His Thr Phe Leu Met
          85             90             95

acc acg gtg acc ttc tgt ggg tca cga aaa atc cac tac atc ttc tgt      337
Thr Thr Val Thr Phe Cys Gly Ser Arg Lys Ile His Tyr Ile Phe Cys
          100            105            110

gag atg tat gta ttg ctg agg ctg gca tgt tcc gac act cag att aat      385
Glu Met Tyr Val Leu Leu Arg Leu Ala Cys Ser Asp Thr Gln Ile Asn
          115            120            125

cac aca gtg ctg att gcc aca ggc tgc ttt atc ttc ctc att ccc ttt      433
His Thr Val Leu Ile Ala Thr Gly Cys Phe Ile Phe Leu Ile Pro Phe
          130            135            140

gga ttc atg atc att tcc tat gtg ttg att gtc aga gcc atc ctc aga      481
Gly Phe Met Ile Ile Ser Tyr Val Leu Ile Val Arg Ala Ile Leu Arg
          145            150            155            160

ata ccc tca gtc tct aag aaa tac aaa gcc ttc tcc act tgt gcc tcc      529
Ile Pro Ser Val Ser Lys Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
          165            170            175

cat ttg ggt gta gtc tcc ctc ttc tat ggg aca ctt cgt atg gta tac      577
His Leu Gly Val Val Ser Leu Phe Tyr Gly Thr Leu Arg Met Val Tyr
          180            185            190

ctg aag ccc ctc cat acc tac tct gtg aag gac tca gta gcc aca gtg      625

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Leu Lys Pro Leu His Thr Tyr Ser Val Lys Asp Ser Val Ala Thr Val
 195 200 205

Met Tyr Ala Val Val Thr Pro
 210 215

<210> 86
 <211> 649
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 86
 c tgg gtt gac atc tgt ttc agc atc tgc atc atc ccc aag atg ctg gtg 49
 Trp Val Asp Ile Cys Phe Ser Ile Cys Ile Ile Pro Lys Met Leu Val
 1 5 10 15
 aac atc cag acc aag aac aaa acc atc tct tac atg gac tgc ctc acc 97
 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
 20 25 30
 cag gtc tat ttc tcc atg ttt ttt cct att ctg gac acg cta ctc ctg 145
 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
 35 40 45
 acc gtg atg gct tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
 50 55 60
 tat gta acc atc atg aac ccc cgc ctc tgc ggc ctc ctg gtt ttt gtc 241
 Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
 65 70 75 80
 acg tgg ctc att ggt gtc atg aca ccc ctc ctc cat att tct ctg ttg 289
 Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu
 85 90 95
 acg cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337
 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
 100 105 110
 gaa ctg aca cac atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385
 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125
 agc acg ttg ata tat gtt atg aca ggt gtg ctg ggc gtt ttt ccc ctc 433
 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
 130 135 140
 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag 481
 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
 145 150 155 160
 atg tcc tca tct ggg gga aaa gag aaa gca ctt tct acc tgt ggc tct 529

[illegible]

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<210> 87
<211> 216
<212> PRT
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9546; gene = MSY7; Accession DDBJ/EMBL/GenBank = AF127872
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<400> 87
Trp Val Asp Ile Cys Phe Ser Ile Cys Ile Ile Pro Lys Met Leu Val
1           5           10           15
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Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr
20 25 30

Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His
50 55 60

Tyr Val Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val
65 70 75 80

Thr Trp Leu Ile Gly Val Met Thr Pro Leu Leu His Ile Ser Leu Leu
85 90 95

Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys
100 105 110

Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu
130 135 140

Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys
145 150 155 160

Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Ile Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His
 180 185 190

Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 88
 <211> 645
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(645)
 <223> Taxon = 9546; gene = MSY8; pseudogene; Accession DDBJ/EMBL/ GenBank = AF127873

<400> 88
 ctttgttgac atctgtttta tctccaccac cgtccccagg atgctgatga acatccaggc 60
 atggagcaaa gacatctcct acgtggggtg cctcactcag gtgtattttt taatgatgtt 120
 tgctggaatg gatactttcc tactggccat gatggcctat gaccggtttg tggccatctg 180
 ccaccccctg cactacacgg tcatcatgaa ccctgcctc tgtggcatcc tggttctggc 240
 atcttgattc atcattttat ggggtctcct agttcatatt ctactgatga agagtttgat 300
 ctccataggc actgagattc cgcatttctt ctgtgaactg gctcagggtcc tcaagggtgcc 360
 cgctctgata ctctcctcgt taacattgtc ttgtatgtgg ccacagcact gctgggtgtg 420
 cttcctgtag ctgggacctt cttctcctac tctcagatcg tctcctcctt aatgagggatg 480
 tcctccaccg agggcaagta caaagccttt tccacctgtg ggtctcacct ctgtgtggtc 540
 tccttgttct atggaacagg acttgggggtc tatctcagtt ctgctgtgac ccattcttcc 600
 cagagcagct ccatggcctc agtgatgtac accatgggtca ccccc 645

<210> 89
 <211> 649
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9546; gene = MSY9; Accession DDBJ/EMBL/GenBank = AF127874

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400>	89
c ttg gct gac atc ggt ttc acc tcc acc aca gtc ccc aag atg ctg gtg	49
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val	
1 5 10 15	
aac atc cag gcg cag agc aat gcc atc agc tat gca ggc tgc atc tcc	97
Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser	
20 25 30	
cag atg tat ttt ttc atg gtt ttt gga ggc ata gac aca ttt ctc ctc	145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu	
35 40 45	
acc gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg tac	193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr	
50 55 60	
tac cct gtc att atg aac ccc cgc ctc tgt ggc ctg ctg gtt ctt gtg	241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val	
65 70 75 80	
tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg	289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met	
85 90 95	
ctg cag ttg tcc ttt tgc acc agt tgg gtc att cag cac ttt tac tgc	337
Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys	
100 105 110	
gag ctt gct cag gcc ctc acg ctt gcc tgc tca gac aca cac atc aat	385
Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn	
115 120 125	
tac atc ctg ctc tac gtg gtg acc ggc ctt ctg ggt ttt gtg ccc ttc	433
Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe	
130 135 140	
tca gga atc ctt ttc tcc tac acc caa att gtc tcc tcc atc ctg aga	481
Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg	
145 150 155 160	
atc tca tcc aca gat ggg aaa cac aaa gcc ttt tct acc tgc gga tct	529
Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser	
165 170 175	
cat ctg tct gtg gtt ttt tta ttc tat ggg aca ggc ctt ggt gtg tat	577
His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr	
180 185 190	
ctt agt tcc aat gca tcg tcc tct tcc tgg cgg ggc atg gtg gcc tcg	625
Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser	
195 200 205	
gtc atg tac act gtg gtc acc ccc	649
Val Met Tyr Thr Val Val Thr Pro	
210 215	
<210>	90
<211>	216
<212>	PRT
<213>	Macaca sylvanus
<220>	
<221>	misc feature

<222> (1)..(649)
 <223> Taxon = 9546; gene = MSY9; Accession DDBJ/EMBL/GenBank = AF127874

<400> 90
 Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Ala Gln Ser Asn Ala Ile Ser Tyr Ala Gly Cys Ile Ser
 20 25 30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Ile Asp Thr Phe Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
 50 55 60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
 65 70 75 80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
 85 90 95

Leu Gln Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
 100 105 110

Glu Leu Ala Gln Ala Leu Thr Leu Ala Cys Ser Asp Thr His Ile Asn
 115 120 125

Tyr Ile Leu Leu Tyr Val Val Thr Gly Leu Leu Gly Phe Val Pro Phe
 130 135 140

Ser Gly Ile Leu Phe Ser Tyr Thr Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Phe Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Arg Gly Met Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 91
 <211> 649
 <212> DNA
 <213> Callithrix jacchus
 <220>

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<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA21; Accession DDBJ/EMBL/GenBank = AF127875

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 91
c ttt gtg gac atc tgt gtt acc tcc acc aca ctt ccg aag aca ctg tca      49
  Phe Val Asp Ile Cys Val Thr Ser Thr Thr Leu Pro Lys Thr Leu Ser
    1             5             10             15

aac atc cag aca cac agc aaa gtc atc acc tat gca ggc tgc gtc acc      97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
          20             25             30

cag ttg tac ttc ttt gta ctc ttc ata ggg ttg gac agc tta ctc ccg      145
Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro
          35             40             45

acc gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50             55             60

tac acg gtc atc atg aac cct cag ttc tgt gga ctg ctg gtt ctg gtg      241
Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val
          65             70             75             80

tcc tgg atc atg agt gcc ctg cat tct ttg aca gaa agc tta atg gta      289
Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val
          85             90             95

tac cca ctg ctc ttt tgt aca gac ttg aaa atc ccc cag ttt ttc tgt      337
Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys
          100            105            110

gaa att cat cag ata att caa ttt gcc tgt tct gac acc ttt ctt aat      385
Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn
          115            120            125

aac ctg gtg atg tat ttg tca act gtg ctc ctg ggc ggt ggt ccc ctt      433
Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Gly Pro Leu
          130            135            140

gct ggg atc ctg tac tct tac tct aag ata gct tcc tct ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
          145            150            155            160

atc tca tca gct gag ggg aag tac aag gca ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
          165            170            175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc cta ggg gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
          180            185            190

ctg agt tct gct gca acc cac agc tca ctc tca agc gca gca gcc tcg      625
Leu Ser Ser Ala Ala Thr His Ser Ser Leu Ser Ser Ala Ala Ala Ser
          195            200            205

gtg atg tac aca gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro
          210            215

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<210> 92
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA21; Accession DDBJ/EMBL/GenBank = AF127875

<400> 92
Phe Val Asp Ile Cys Val Thr Ser Thr Thr Leu Pro Lys Thr Leu Ser
1          5          10          15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
20          25          30

Gln Leu Tyr Phe Phe Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Pro
35          40          45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50          55          60

Tyr Thr Val Ile Met Asn Pro Gln Phe Cys Gly Leu Leu Val Leu Val
65          70          75          80

Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Val
85          90          95

Tyr Pro Leu Leu Phe Cys Thr Asp Leu Lys Ile Pro Gln Phe Phe Cys
100         105         110

Glu Ile His Gln Ile Ile Gln Phe Ala Cys Ser Asp Thr Phe Leu Asn
115         120         125

Asn Leu Val Met Tyr Leu Ser Thr Val Leu Leu Gly Gly Gly Pro Leu
130         135         140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
145         150         155         160

Ile Ser Ser Ala Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165         170         175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
180         185         190

Leu Ser Ser Ala Ala Thr His Ser Ser Leu Ser Ser Ala Ala Ala Ser
195         200         205

Val Met Tyr Thr Val Val Thr Pro
210         215

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<210> 93
<211> 649
<212> DNA
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 93
c ttg gtt gac atc tgt ttc acc tcc acc aca gtc ccc aag att ctg gtg      49
  Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Ile Leu Val
    1             5             10             15

aac atc cag gag cag agt ggt acc atc agc tat gca ggc tgc att gcc      97
Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
          20             25             30

cag atg tat ttt ttc atg gtt ttt gga ggc atg gac aca ttt ctc ctc      145
Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
          35             40             45

act gtg atg gcc tat gac cgg tat gtg gct atc tgt cac ccc ctg tcc      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
          50             55             60

tac cct gtc att gta aac ccc cgc ctc tgc ggc ctg ttg gtt ctt gtg      241
Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
          65             70             75

tcc tgg ttc ctc agc ttg tca tac tcc ctg atc cag agt ctg ttg atg      289
Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
          85             90             95

ctg cgg cta tcc ttc tgc acc agt tgg gtc att cag cac ttt tac tgt      337
Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
          100            105            110

gag ctt gct cag gtt ctc acg ctt gcc tgc tca gac aca cat gtc aat      385
Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
          115            120            125

tac atc ctg ctc tac atg gtg acc ggc ctt ctg ggc tgt gtt ccc ttc      433
Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
          130            135            140

tca ggg atc ctt ttc tcc tac atc caa att gtc tcc tcc atc ctg aga      481
Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
          145            150            155

atc cca tcc aca gat ggg aaa cat aaa gcc ttt tct acc tgt gga tct      529
Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
          165            170            175

cat ctg tct gtg gtt tct tta ttc tac ggg aca ggc ctt ggt gtc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
          180            185            190

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ctt agc tcc aat gcc tcg tcc tct tcc tgg tgg ggc atg gtg gcc tca      625
Leu Ser Ser Asn Ala Ser Ser Ser Ser Trp Trp Gly Met Val Ala Ser
      195                      200                      205

gcc atg tac aca gtg gtc acc cct      649
Ala Met Tyr Thr Val Val Thr Pro
      210                      215

<210> 94
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA22; Accession DDBJ/EMBL/GenBank = AF127876

<400> 94
Leu Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Ile Leu Val
1                      5                      10                      15

Asn Ile Gln Glu Gln Ser Gly Thr Ile Ser Tyr Ala Gly Cys Ile Ala
      20                      25                      30

Gln Met Tyr Phe Phe Met Val Phe Gly Gly Met Asp Thr Phe Leu Leu
      35                      40                      45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Ser
      50                      55                      60

Tyr Pro Val Ile Val Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Val
65                      70                      75                      80

Ser Trp Phe Leu Ser Leu Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
      85                      90                      95

Leu Arg Leu Ser Phe Cys Thr Ser Trp Val Ile Gln His Phe Tyr Cys
      100                      105                      110

Glu Leu Ala Gln Val Leu Thr Leu Ala Cys Ser Asp Thr His Val Asn
      115                      120                      125

Tyr Ile Leu Leu Tyr Met Val Thr Gly Leu Leu Gly Cys Val Pro Phe
      130                      135                      140

Ser Gly Ile Leu Phe Ser Tyr Ile Gln Ile Val Ser Ser Ile Leu Arg
145                      150                      155                      160

Ile Pro Ser Thr Asp Gly Lys His Lys Ala Phe Ser Thr Cys Gly Ser
      165                      170                      175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
      180                      185                      190

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Leu Ser Ser Asn Ala Ser Ser Ser Trp Trp Gly Met Val Ala Ser
 195 200 205

Ala Met Tyr Thr Val Val Thr Pro
 210 215

<210> 95
 <211> 649
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA23; Accession DDBJ/EMBL/GenBank = AF127877

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 95
 t ttc acg gat atc tgc ttc aca aca gtc ata gtg ccc agg atg ctg gtg 49
 Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
 1 5 10 15
 aat ttt cta tca ggg aca aag gtt atc ccc tac atg ggc tgc ctg gtc 97
 Asn Phe Leu Ser Gly Thr Lys Val Ile Pro Tyr Met Gly Cys Leu Val
 20 25 30
 caa atg tac ttc ttc atg gcc ttt ggg aac act gac agc tac ctg ctg 145
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
 35 40 45
 gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac 193
 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60
 tat gat gtg gct atg aac ccc cgg cat tgc cta ctc atg cta ttg ggt 241
 Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Leu Gly
 65 70 75 80
 tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg 289
 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95
 tct cac ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt 337
 Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
 100 105 110
 gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc 385
 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125
 cag atg gtg gtc atg act gag act tta gct gtc att gtg acc ccc ttc 433
 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140
 ctg tgt atc atc ttc tcc tac ctg cga atc atc atc act gtg ctc aga 481
 Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
 145 150 155 160

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atc ccc ttt gca gct ggg aag tgg agg gcc ttc tct acc tgt ggc tcc      529
Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
                      165                      170                      175

cac ctc act gta gta gcc ctt ttc tac ggg agt ata tat tat gtc tat      577
His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr
                      180                      185                      190

ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca      625
Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
                      195                      200                      205

gtt atg tac aca gta gtg aca ccc      649
Val Met Tyr Thr Val Val Thr Pro
                      210                      215

<210> 96
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA23; Accession DDBJ/EMBL/GenBank = AF127877

<400> 96
Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
1                      5                      10                      15

Asn Phe Leu Ser Gly Thr Lys Val Ile Pro Tyr Met Gly Cys Leu Val
                20                      25                      30

Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Thr Asp Ser Tyr Leu Leu
                35                      40                      45

Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
                50                      55                      60

Tyr Asp Val Ala Met Asn Pro Arg His Cys Leu Leu Met Leu Leu Gly
65                      70                      75                      80

Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
                85                      90                      95

Ser His Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
                100                      105                      110

Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
                115                      120                      125

Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
                130                      135                      140

Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
145                      150                      155                      160

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Ile Pro Phe Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Tyr Tyr Val Tyr
180 185 190

Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 97

<211> 649

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 9483; gene = CJA24; Accession DDBJ/EMBL/GenBank = AF127878

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 97

c ttt gta gac atc tgt ttt gtg tct acc act gtc cca aag atg ctg gta 49
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
20 25 30

cag ata ggc cat tgc cta ctc ttt gca gta ttg gac gtc ttt atg ctg 145
Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac 193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg 289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100 105 110

gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat 385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115 120 125

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gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt      433
Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
   130                               135                               140

gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
   145                               150                               155                               160

atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
                               165                               170                               175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac      577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
                               180                               185                               190

ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg      625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
                               195                               200                               205

gtg atg tac act gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro
   210                               215

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<210> 98
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA24; Accession DDBJ/EMBL/GenBank = AF127878

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<400> 98
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1                               5                               10                               15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
                20                               25                               30

Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
35                               40                               45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50                               55                               60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65                               70                               75                               80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85                               90                               95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
100                               105                               110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
115                               120                               125

```

Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
130 135 140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 99
<211> 649
<212> DNA
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA25; Accession DDBJ/EMBL/GenBank = AF127879

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 99
c ttt gct gac atc tgt ttc aca tcc acg acc gtc cca aag atg ctg gtg 49
Phe Ala Asp Ile Cys Phe Thr Ser Thr Val Pro Lys Met Leu Val
1 5 10 15

gat atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc 97
Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
20 25 30

cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg 145
Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
35 40 45

acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac 193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg 241
Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
65 70 75 80

tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att 289
Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
85 90 95

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ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt      337
Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
               100                      105                      110

gat gtt ctg gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat      385
Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
               115                      120                      125

aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctg      433
Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
               130                      135                      140

tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga      481
Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
               145                      150                      155                      160

gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct      529
Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
               165                      170                      175

cac ctg tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat      577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
               180                      185                      190

ctc agt ctt gca gct aca cca tct tct agg aca agt ctg atg gcc tcg      625
Leu Ser Leu Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
               195                      200                      205

gtg atg tac acc atg gtc acc ccc                                     649
Val Met Tyr Thr Met Val Thr Pro
               210                      215

<210> 100
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA25; Accession DDBJ/EMBL/GenBank = AF127879

<400> 100
Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1              5              10              15

Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
                20              25              30

Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
35              40              45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50              55              60

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
65              70              75              80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
85              90              95

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tat	cca	gtc	atc	atg	agc	cca	cga	ctc	tgt	ggc	ttc	tta	gtg	ttg	gtg	241
Tyr	Pro	Val	Ile	Met	Ser	Pro	Arg	Leu	Cys	Gly	Phe	Leu	Val	Leu	Val	
65				70					75					80		
tct	gct	ttt	ctt	agc	ctt	tta	ata	tcc	cag	gtg	cac	aat	ttg	att	gtc	289
Ser	Ala	Phe	Leu	Ser	Leu	Leu	Ile	Ser	Gln	Val	His	Asn	Leu	Ile	Val	
			85					90					95			
tta	caa	ttt	tct	tgc	ttc	aaa	gat	ata	aag	att	tct	aat	ttc	ttc	tgt	337
Leu	Gln	Phe	Ser	Cys	Phe	Lys	Asp	Ile	Lys	Ile	Ser	Asn	Phe	Phe	Cys	
		100					105					110				
gac	cct	tct	caa	ctc	ctc	aca	ctt	gct	tgt	tcc	gac	acg	ttt	gtc	aat	385
Asp	Pro	Ser	Gln	Leu	Leu	Thr	Leu	Ala	Cys	Ser	Asp	Thr	Phe	Val	Asn	
	115					120					125					
aac	aac	ata	gtc	atg	aat	ttc	ttt	gct	gct	gta	ttt	ggg	ttt	ctt	ccc	433
Asn	Asn	Ile	Val	Met	Asn	Phe	Phe	Ala	Ala	Val	Phe	Gly	Phe	Leu	Pro	
	130				135					140						
atc	tca	ggg	atc	ttt	ttg	tct	tac	tat	aaa	att	gtt	tcc	tcc	att	ctg	481
Ile	Ser	Gly	Ile	Phe	Leu	Ser	Tyr	Tyr	Lys	Ile	Val	Ser	Ser	Ile	Leu	
145				150					155					160		
aga	gtt	cca	tca	tca	agt	ggg	aag	tat	aaa	gcc	ttc	tct	acc	tgt	agc	529
Arg	Val	Pro	Ser	Ser	Ser	Gly	Lys	Tyr	Lys	Ala	Phe	Ser	Thr	Cys	Ser	
			165				170						175			
tct	cac	ctg	gca	gtt	gtt	tgc	tta	ttt	tat	gga	aca	gtc	ctt	gga	gtg	577
Ser	His	Leu	Ala	Val	Val	Cys	Leu	Phe	Tyr	Gly	Thr	Val	Leu	Gly	Val	
		180					185					190				
tac	ctt	ggg	tca	tca	gtg	tca	tcc	ccc	agg	aag	aga	gtg	gtg	acc	tca	625
Tyr	Leu	Gly	Ser	Ser	Val	Ser	Ser	Pro	Arg	Lys	Arg	Val	Val	Thr	Ser	
	195					200					205					
gtg	atg	tac	aca	gtg	gtc	act	ccc									649
Val	Met	Tyr	Thr	Val	Val	Thr	Pro									
	210				215											
<210>	102															
<211>	216															
<212>	PRT															
<213>	Callithrix jacchus															
<220>																
<221>	misc_feature															
<222>	(1)..(649)															
<223>	Taxon = 9483; gene = CJA26; Accession DDBJ/EMBL/GenBank = AF127880															
<400>	102															

Tyr Pro Val Ile Met Ser Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

Ser Ala Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

Leu Gln Phe Ser Cys Phe Lys Asp Ile Lys Ile Ser Asn Phe Phe Cys
100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ala Cys Ser Asp Thr Phe Val Asn
115 120 125

Asn Asn Ile Val Met Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro
130 135 140

Ile Ser Gly Ile Phe Leu Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu
145 150 155 160

Arg Val Pro Ser Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser
165 170 175

Ser His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Leu Gly Val
180 185 190

Tyr Leu Gly Ser Ser Val Ser Ser Pro Arg Lys Arg Val Val Thr Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 103
<211> 649
<212> DNA
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA62; Accession DDBJ/EMBL/GenBank = AF127881

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 103
c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag acg ctg gta 49
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Thr Leu Val
1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
20 25 30

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cag ata ggc cat tgc ctc ctc ttt gca gta ttg gac gtc ttt atg ctg      145
Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
      35                        40                        45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac cca ctg cac      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50                        55                        60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca      241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
      65                        70                        75                        80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg      289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
      85                        90                        95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
      100                       105                       110

gta ctt aat cag gtc atc cac ctt gcc tgt tct gac act ttt ctt aat      385
Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
      115                       120                       125

gat gtg gtg atg tat ttg gcc gct gtg ctg ctg ggg ggt ggt ccc ctt      433
Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
      130                       135                       140

gca ggg att ctt tac tct tac tct aag ata gtt tcc tcc ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
      145                       150                       155                       160

atc tca tca gct cag ggg aag tac aag gca ttt tcc acc tgt gta tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
      165                       170                       175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac      577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
      180                       185                       190

ctt agt tct gct gca act ggc aac tca cat tca aga gct gca gcc tcg      625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
      195                       200                       205

gtg atg tac act gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
      210                       215

<210> 104
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA62; Accession DDBJ/EMBL/GenBank = AF127881

<400> 104
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Thr Leu Val
1                        5                        10                        15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
      20                        25                        30

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Gln Ile Gly His Cys Leu Leu Phe Ala Val Leu Asp Val Phe Met Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
 85 90 95
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110
 Val Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asn
 115 120 125
 Asp Val Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Pro Leu
 130 135 140
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
 165 170 175
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Arg Ala Ala Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 105
 <211> 649
 <212> DNA
 <213> Callithrix jacchus

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882

 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

 <400> 105

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t ttc acg gat atc tgc ttc aca aca gtc ata gtg ccc agg atg ctg gtg      49
Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
1          5          10          15

aat ttt cta tca gag aca aag gtt atc tcc tac atg ggc tgc ctg gtc      97
Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val
          20          25          30

cca atg tac ttc ttc atg gcc ttt gcg aac act gac agc tac ctg ctg      145
Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu
          35          40          45

gcc tct atg gcc atc gac cgg ctg gtg gcc atc tgc aac ccc tta cac      193
Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
          50          55          60

tat gat gtg gct atg aac tcc cgg cgt tgc cta ctc atg cta ttg ggt      241
Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly
65          70          75          80

tct tgc agc atc tcc cac cta cat tcc ctg ttc cgg gtg cta ctt atg      289
Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
          85          90          95

tct cgc ctg tct ttc tgt gcc tcc cac gtc att aag cac ttt ttc tgt      337
Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
          100          105          110

gac acc cag cct gtg cta aag ctg tcc tgc tct gac acg tcc tcc agc      385
Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
          115          120          125

cag atg gtg gtc atg act gag acc tta gct gtt att gtg acc ccc ttc      433
Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
          130          135          140

ctg tgt atc atc ttc tcc tac ctg cga atc atc atc act gtg ctc aga      481
Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
145          150          155          160

atc ccc tct gca gcc ggg aag tgg agg gcc ttc tct acc tgt ggc tcc      529
Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
          165          170          175

cac ctc act gta gta gcc ctt ttc tac ggg agt att att tat gtc tat      577
His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
          180          185          190

ttt agg ccc ctg tcc atg tac tca gtg gtg aag gac cga gta gcc aca      625
Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
          195          200          205

gtt atg tac aca gta gtg aca ccc
Val Met Tyr Thr Val Val Thr Pro      649
210          215

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<210> 106
<211> 216
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9483; gene = CJA80; Accession DDBJ/EMBL/GenBank = AF127882

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<400> 106
 Phe Thr Asp Ile Cys Phe Thr Thr Val Ile Val Pro Arg Met Leu Val
 1 5 10 15

 Asn Phe Leu Ser Glu Thr Lys Val Ile Ser Tyr Met Gly Cys Leu Val
 20 25 30

 Pro Met Tyr Phe Phe Met Ala Phe Ala Asn Thr Asp Ser Tyr Leu Leu
 35 40 45

 Ala Ser Met Ala Ile Asp Arg Leu Val Ala Ile Cys Asn Pro Leu His
 50 55 60

 Tyr Asp Val Ala Met Asn Ser Arg Arg Cys Leu Leu Met Leu Leu Gly
 65 70 75 80

 Ser Cys Ser Ile Ser His Leu His Ser Leu Phe Arg Val Leu Leu Met
 85 90 95

 Ser Arg Leu Ser Phe Cys Ala Ser His Val Ile Lys His Phe Phe Cys
 100 105 110

 Asp Thr Gln Pro Val Leu Lys Leu Ser Cys Ser Asp Thr Ser Ser Ser
 115 120 125

 Gln Met Val Val Met Thr Glu Thr Leu Ala Val Ile Val Thr Pro Phe
 130 135 140

 Leu Cys Ile Ile Phe Ser Tyr Leu Arg Ile Ile Ile Thr Val Leu Arg
 145 150 155 160

 Ile Pro Ser Ala Ala Gly Lys Trp Arg Ala Phe Ser Thr Cys Gly Ser
 165 170 175

 His Leu Thr Val Val Ala Leu Phe Tyr Gly Ser Ile Ile Tyr Val Tyr
 180 185 190

 Phe Arg Pro Leu Ser Met Tyr Ser Val Val Lys Asp Arg Val Ala Thr
 195 200 205

 Val Met Tyr Thr Val Val Thr Pro
 210 215

 <210> 107
 <211> 649
 <212> DNA
 <213> Callithrix jacchus

 <220>
 <221> misc_feature
 <222> (1)..(649)

<223> Taxon = 9483; gene = CJA81; Accession DDBJ/EMBL/GenBank = AF127883

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 107

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c ttt gct gac atc tgc ttc aca tcc acg acc gtc cca aag atg ctg gtg      49
  Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
    1             5             10             15

gat atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc      97
Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
          20             25             30

cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg     145
Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
      35             40             45

acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac     193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
      50             55             60

tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg     241
Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
      65             70             75             80

tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att     289
Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
          85             90             95

ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt     337
Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
      100             105             110

gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat     385
Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
      115             120             125

aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc     433
Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
      130             135             140

tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga     481
Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
      145             150             155             160

gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct     529
Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
          165             170             175

cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat     577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
          180             185             190

ctc agt tct gca gct aca cca tct tct agg aca agt ctg atg gcc tcg     625
Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
          195             200             205

gtg atg tac acc atg gtc acc ccc                                     649
Val Met Tyr Thr Met Val Thr Pro
      210             215
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<210> 108

<211> 216
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA81; Accession DDBJ/EMBL/GenBank = AF127883

<400> 108

Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asp Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30

Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
 65 70 75 80

Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110

Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
 115 120 125

Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
 130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160

Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
 195 200 205

Val Met Tyr Thr Met Val Thr Pro
 210 215

<210> 109
 <211> 649
 <212> DNA
 <213> *Callithrix jacchus*

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9483; gene = CJA82; Accession DDBJ/EMBL/GenBank = AF127884

 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

 <400> 109
 c ttt gct gac atc tgt ttc aca tcc acg acc gtc cca aag atg ctg gtg 49
 Phe Ala Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

 ggt atc caa aca caa agc aaa atg atc act ttt gca ggg tgc ctc acc 97
 Gly Ile Gln Thr Gln Ser Lys Met Ile Thr Phe Ala Gly Cys Leu Thr
 20 25 30

 cag att ttt ttt ttc gtt gca ttt gga tgc ctg gac aat ttg ctc ttg 145
 Gln Ile Phe Phe Phe Val Ala Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45

 acc gtg atg gcc tat gac cgg ttc gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

 tac gcg gtc atc atg aac ccc cgg ctc tgt aga ctg cta gtt ctg ggg 241
 Tyr Ala Val Ile Met Asn Pro Arg Leu Cys Arg Leu Leu Val Leu Gly
 65 70 75 80

 tcc tgg tgc atc agt gtc atg gtt tct ctg ctc gag acc ttg acc att 289
 Ser Trp Cys Ile Ser Val Met Val Ser Leu Leu Glu Thr Leu Thr Ile
 85 90 95

 ttg agg ctg tcc ttc tgc aca aac atg gaa atc cca cac ttt ttt tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110

 gat gtt ctc gaa gtc ctg aag ctc gcc tgt tct gaa acc ctc gtc aat 385
 Asp Val Leu Glu Val Leu Lys Leu Ala Cys Ser Glu Thr Leu Val Asn
 115 120 125

 aaa atc gtg atg tat ttt gtg aca att gca atg ggt gtt ttt cct ctc 433
 Lys Ile Val Met Tyr Phe Val Thr Ile Ala Met Gly Val Phe Pro Leu
 130 135 140

 tct gga atc cta tac tct tat tct cag att ttc tcc tcc atc ctg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Ser Gln Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160

 gta tca cct gcc caa ggc cag cac aaa gcc ttt tcc acc tgt ggg tct 529
 Val Ser Pro Ala Gln Gly Gln His Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

 cac ctc tca gtg gtc acc ctg ttc tat ggc acg ggc ctt ggg gta tat 577
 His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

 ctc agt tct gca gct aca cca tct tct agg aca agt ctg atg gcc tcg 625
 Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser

Leu Ser Ser Ala Ala Thr Pro Ser Ser Arg Thr Ser Leu Met Ala Ser
 195 200 205

Val Met Tyr Thr Met Val Thr Pro
 210 215

<210> 111
 <211> 658
 <212> DNA
 <213> Pongo pygmaeus

<220>
 <221> misc_feature
 <222> (1)..(658)
 <223> Taxon = 9600; gene = PPY10; pseudogene; Accession DDBJ/EMBL/GenBank = AF127885

<400> 111
 cttgcctgac atcggtttca cctcccgcat ggtccccaag atgattgtgg acatccaatc 60
 tcacagcaga gtcatttctc aggcaggcta cctgactcag atgtctctct ttgccatttt 120
 tggaggcgtg gaagagagac atgctcctga gtgtgaaggc ctatgaccgg tttgtagcca 180
 cctgtcacc cctgtatcat tcagccatca tgaagtcattg tttctgtggc tttctagttt 240
 tgttgtcttt tttttttctc tcagtctttt agacgcccaa ctgcacaact tgattgcctt 300
 gcaaattggc tgctttgagg atgtggaaat ttctaatttc ttctgtgacc cttctcaact 360
 ccccatcttg catgttgtga cagcttcacc gataacatca tcacgtatct ccctgacgcc 420
 atatccccct ttattcccat ctgggggacc cttttctcta taatatcaaa ttgtttcctc 480
 cattctgagg gcttcatcat cagggtgggag gtataaagcc ttctccatct gtgggtctca 540
 cctgtcagtt gtttgcttat tttatggaac aggcataatg ggggtacctca gttcagatgt 600
 gtcattcttc ctgagaaagg ctgcagtgcac ctcagtgatg tacaccgtgg tcaccccc 658

<210> 112
 <211> 649
 <212> DNA
 <213> Pongo pygmaeus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9600; gene = PPY11; Accession DDBJ/EMBL/GenBank = AF127886

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 112
 c ttg gct gac atc ggt ttc acc tcc acc acg gtc ccc aag atg att gtg 49
 Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
 1 5 10 15
 gac atg caa act cac agc aga gtc atc tcc tat gca ggc tgc ctg act 97
 Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr
 20 25 30

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cag atg tct ttt ttt gtc ctt ttt gca tgt atg gat gac atg ctt ctg      145
Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu
      35              40              45

agt gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac cct ccg gat      193
Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp
      50              55              60

tac cca gtt acc atg aac cca tgt ttc tgt ggc ttc cta gtt ttg ttg      241
Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu
      65              70              75

tct ttt ttt ctc agt ctt tta gac tcc cag ctg cac aat tgg att gcc      289
Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala
      85              90              95

tta caa att acc tgc ttc aag gat gtg gaa att ccc aat ttc ttc tgt      337
Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys
      100              105              110

gac cct tcc caa ctc ccc cac ctt gcc tgt tgt gac acc ttc acc aat      385
Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn
      115              120              125

gac ata gtc atg tat ttc ctt gct gcc ata ttt ggt ttt ctt ccc atc      433
Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile
      130              135              140

ttg ggg atc ctt ttc tct tac tat aaa att gtt tcc tcc att ctg agg      481
Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg
      145              150              155

gtt tca tca tca ggt ggg agg tat aaa gcc ttc gcc acc tgt ggc tct      529
Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser
      165              170              175

cac ctg tca gtt gtt tgc tta ttt tat gga aca gcc ctt gga ggg tac      577
His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr
      180              185              190

ctc agt tca gac atg tcc tct tat ccc aga aag ggt gca gtg gct tca      625
Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser
      195              200              205

gtg atg tac aca gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro      649
      210              215

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<210> 113
<211> 216
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY11; Accession DDBJ/EMBL/GenBank = AF127886

<400> 113
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Lys Met Ile Val
1              5              10              15

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Asp Met Gln Thr His Ser Arg Val Ile Ser Tyr Ala Gly Cys Leu Thr

097475-03001

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                20                25                30

Gln Met Ser Phe Phe Val Leu Phe Ala Cys Met Asp Asp Met Leu Leu
    35                40                45

Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Pro Asp
    50                55                60

Tyr Pro Val Thr Met Asn Pro Cys Phe Cys Gly Phe Leu Val Leu Leu
    65                70                75                80

Ser Phe Phe Leu Ser Leu Leu Asp Ser Gln Leu His Asn Trp Ile Ala
    85                90                95

Leu Gln Ile Thr Cys Phe Lys Asp Val Glu Ile Pro Asn Phe Phe Cys
    100                105                110

Asp Pro Ser Gln Leu Pro His Leu Ala Cys Cys Asp Thr Phe Thr Asn
    115                120                125

Asp Ile Val Met Tyr Phe Leu Ala Ala Ile Phe Gly Phe Leu Pro Ile
    130                135                140

Leu Gly Ile Leu Phe Ser Tyr Tyr Lys Ile Val Ser Ser Ile Leu Arg
    145                150                155                160

Val Ser Ser Ser Gly Gly Arg Tyr Lys Ala Phe Ala Thr Cys Gly Ser
    165                170                175

His Leu Ser Val Val Cys Leu Phe Tyr Gly Thr Ala Leu Gly Gly Tyr
    180                185                190

Leu Ser Ser Asp Met Ser Ser Tyr Pro Arg Lys Gly Ala Val Ala Ser
    195                200                205

Val Met Tyr Thr Val Val Thr Pro
    210                215

<210> 114
<211> 654
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(654)
<223> Taxon = 9600; gene = PPY12; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127887

<400> 114
cttgccctgaa atcggtttca cctccaccac gatccccaag attgtggaca tccaatctca        60
cagcagagtc atctcctctg caggcttgcc tgactcagat gtctctttgc catttttgga        120

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115          120          125
aac att gtc ttg tat gtg gcc acg gca ctg ctg ggt gtg ttt cct gta 433
Asn Ile Val Leu Tyr Val Ala Thr Ala Leu Leu Gly Val Phe Pro Val
130          135          140

gct ggg atc ctc ttc tcc tac tct cag atc gtc tcc tcc tta atg aga 481
Ala Gly Ile Leu Phe Ser Tyr Ser Gln Ile Val Ser Ser Leu Met Arg
145          150          155          160

atg tcc tcc acc gag gcc aag tac aaa gcc ttt tcc acc tgt gga tct 529
Met Ser Ser Thr Glu Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165          170          175

cac ctc tgt gtg gtc tcc ttg ttc aat gga aca gga ctt ggg gtc tat 577
His Leu Cys Val Val Ser Leu Phe Asn Gly Thr Gly Leu Gly Val Tyr
180          185          190

ctc agt tct gct gtg acc cat tct tcc cag agc agc tcc atg gcc tca 625
Leu Ser Ser Ala Val Thr His Ser Ser Gln Ser Ser Ser Met Ala Ser
195          200          205

gtg atg tat gcc atg gtc acc ccc 649
Val Met Tyr Ala Met Val Thr Pro
210          215

<210> 116
<211> 216
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY49; Accession DDBJ/EMBL/GenBank = AF127888

<400> 116
Phe Val Asp Thr Cys Phe Ile Ser Thr Thr Val Pro Lys Met Leu Val
1          5          10          15

Asn Ile Gln Ala Arg Ser Lys Glu Ile Ser Tyr Met Gly Cys Leu Thr
20          25          30

Gln Val Tyr Phe Leu Met Met Phe Ala Gly Met Asp Thr Phe Leu Leu
35          40          45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Gln
50          55          60

Tyr Ala Val Ile Met Asn Pro His Leu Cys Gly Leu Leu Val Leu Ala
65          70          75          80

Ser Trp Phe Ile Ile Phe Trp Val Ser Leu Val His Ile Leu Leu Met
85          90          95

Lys Arg Leu Thr Phe Ser Thr Gly Thr Glu Ile Pro His Phe Phe Cys
100          105          110

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<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 9600; gene = PPY51; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127890

<400> 118
ctttgctgac atctgttttg tgtctagcac tctaccaaag atgctggtga atatccagac      60
acacagcaaa gtcatcacct atgcaggctg catcaccag gtgtgctttt tcgtattctt      120
tgcaggattg gacatctttc tcctgactgt gatggcctat gacggtttgt ggccatctgt      180
cacccccctgc actacacggt catcatgagc cccaggctct gtggactgct ggttctggca      240
tcctggatca tgagtgcctt gaattccttg ctacaaagct taatagtact gcggctttcc      300
ttctgcacag atttggaat cccccacttt ttctgtgaac ttaatcaggt caccacactt      360
gcctgttctg acacctttct taacgacatg gtgatgtatt tgtcatctgc gttgtggggc      420
ggtgtcccc tcactgggat cctttactct tactctaaga ttgtttcttc catacgtgca      480
atctcatcag ctcaggggaa gtacaaggca ttttccacct atgcgtctca cctctcagtt      540
gtctccttat tttatggtac actcctaggg gtgtacctta gttctgctgc aaccacaac      600
tcatactcaa gtgctgcagc ctcggtgatg tacactgtgg tcaccccc      648

<210> 119
<211> 660
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(660)
<223> Taxon = 9600; gene = PPY52; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF127891

<400> 119
cttgccctgac atcagtttca cctccaccac ggtccccaag atgattgtgg acatccaatc      60
tcacagcaga gtcattctct atgcaggctg cctgactcag atgtgtctcc tggccatttt      120
tggaggcatg gaagagagac atgctcctga gtgtgatggc ctatgagcgg tttgtagccc      180
tctgtcacc cctatatcgt tcagccatct tgaaccctg tttctgtggc ttcttagatt      240
tgtgggtctt gttttctttt tcctcagttt ttttagactcc cagctgcgca acttgattgc      300
cttacgcatg acctgcttca aggatgtgga aattcctaata ttcttctggg aaccttctca      360
actcccccat cttacatttt gtgacacctt caccagtaac atccacatgt atttccctgc      420
tgccgtattt ggttttcttc ccatctcggg ggcccttttc tcttacggta aaattgtttc      480
ctccattctg agggtttcat catcagggtg gaagtatcaa ccttctccac ctgtgggtct      540
cacctgtcag ttgtttgctg attttacgga acaggcgttg gagggtagct gggttcagat      600
gtgtcatccc ccccgagaaa ggggtgcagt gcctcagtga tgtacacggt ggtcaccccc      660

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<210> 120
 <211> 633
 <212> DNA
 <213> Pongo pygmaeus

 <220>
 <221> misc_feature
 <222> (1)..(633) <223> Taxon = 9600; gene = PPY76; pseudogene; Accession
 DDBJ/EMBL/ GenBank = AF127892

<400> 120
 cttgcctgac attggtttca ccttggccac ggtccccaag atgattgtag acatgcaatc 60
 acatagcaaaa gtcattctccc atgcgggctg tctgacacag atatctttct ttgtcctttt 120
 tgcattgtata gatgacatgc tctgactgt gatggcctat gactgattcg tggccatctg 180
 tcacccctg aactaccag tcattcatgaa tctcaccctc tgtgtcttct tagtgttggt 240
 gtctttttcc ttagcctgtt ggattcccag ctgcacaatt ggattgttac aattcacctg 300
 cttcaagaat gtggaaatct ttaattttgt ctgtgactga tctcaacctt gcctgttctg 360
 actgtgtcat cagtaacata ttcatacatt tagatagtag aatacttggt tttcttccca 420
 tttcagggat ccttttgtct tactataaaa ttgtgcctc cattctaaga attccattgt 480
 cagatgggaa gtataaagcc ttctccacct gtggctctca cctggcaatt gtttgcattat 540
 tttatggaac aggcatttgt gtgtacctga cttcagctgt gtcactatcc cccaggaatg 600
 gtgtggtcag tgttgtatgt tgtggccacc ccc 633

<210> 121
 <211> 648
 <212> DNA
 <213> Pongo pygmaeus

 <220>
 <221> misc_feature
 <222> (1)..(648)
 <223> Taxon = 9600; gene = PPY77; pseudogene; Accession DDBJ/EMBL/GenBank =
 AF127893

<400> 121
 ctttgctgac ctctgtttta cctccacaac cgtcccaaag atgctactga atatactgac 60
 acagaacaaa ttcataacat atgcaggctg tctcggtcag attttctttt tcaacttcatt 120
 tggatgcctg gacaatttac tcttgaccgt gatggcctat gaccgcttca tggccatctg 180
 tcacccctg cactacacac ggtcatcatg aaccaccagc tctgtggact gctggttcta 240
 gggtcctagt gcatcagtgt catgggtccc tgctcaagac cttgactgtt ttgaggctgt 300
 cctctgcaca aaatggaaat tccacacttt ttttgtgac ttcttgaagt cctgaagctc 360
 gcctgttctg acaccttcatt caataacgta gtgatatact ttgcaactgg catcctgggt 420
 gtgattccct tcaactggaat acttttctct tactataaaa ttgttttctc tatactgagg 480
 atttcctcag ctgggagaaa gtgcaaagcg ttttccacct gtggttccca cctctcagtg 540
 gtcagcttgt tctatggcac aggttttggg gtctatctca gttctgcagc tacaccatct 600

[illegible]

648

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<210> 122
<211> 660
<212> DNA
<213> Pongo pygmaeus
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<220>
<221> misc_feature
<222> (1)..(660)
<223> Taxon = 9600; gene = PPY78; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127894
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[illegible]

```
<210> 123
<211> 649
<212> DNA
<213> Pongo pygmaeus
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<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY85; pseudogene; Accession DDBJ/EMBL/GenBank =
AF127855
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[illegible]

gagttcgctc ttcaggtggg aagtataaag ccttctccac ctgcagctct cacctgtcag 540
 ttgtttgctt attttatgga acagcccttg gagggtagct cagttcagct gtgtcccttt 600
 cctccaggaa ggggtgcagtg gcctcagtga tgtacctggt ggtcacccc 649

<210> 124
 <211> 649
 <212> DNA
 <213> Pongo pygmaeus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9600; gene = PPY9; Accession DDBJ/EMBL/GenBank = AF127896

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 124
 c ttt gta gac atc tgt ttt gcc tct acc acg gtc cca aag atg ctg gtg 49
 Phe Val Asp Ile Cys Phe Ala Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aat atc cag gca cag agc aaa gtt atc acc tat gca ggc tgc atc acc 97
 Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
 20 25 30
 cag atg tac ttt ttc aca cat ttt gta gga ttg gac agc ttc ctc cta 145
 Gln Met Tyr Phe Phe Thr His Phe Val Gly Leu Asp Ser Phe Leu Leu
 35 40 45
 act gtg atg gcc tat gac cgg ttt gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac acg gtc atc atg aac cct caa ctc tgt gga ttg ctg gtt ctg gcg 241
 Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80
 tcc tgg atc atg agt gtc ttg cat tcc tta tta caa agc tta atg gtg 289
 Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val
 85 90 95
 ctg cgg ttg tcc tta tgc aga gag ttg gaa atc ccc cac ttt ttc tgc 337
 Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Phe Cys
 100 105 110
 gaa ctt aat cag gtc atc cac ctt gcc tgt tct gac acc ttt ctt gat 385
 Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp
 115 120 125
 gac atg gtg atg tat ttg gca gct gtg ctg ctg ggt ggg gga tgt ctc 433
 Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Cys Leu
 130 135 140
 gct ggg atc ctt tac tcc tac tct aag ata gtt tcc tcc ata tgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala
 145 150 155 160
 atc tca tca gct caa ggg aag tat aag gca ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser

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                                165                                170                                175
cac ctc tca gtt gtc tcc ttg ttt tat tgt acg agc cta gga gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
                                180                                185                                190

ctt agc tcg gct gca atc cac aac tca cac tca agt gca ata gcc tca      625
Leu Ser Ser Ala Ala Ile His Asn Ser His Ser Ser Ala Ile Ala Ser
                                195                                200                                205

gtg atg tac acc gtg gtc acc ccc      649
Val Met Tyr Thr Val Val Thr Pro
                                210                                215

<210> 125
<211> 216
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9600; gene = PPY9; Accession DDBJ/EMBL/GenBank = AF127896

<400> 125
Phe Val Asp Ile Cys Phe Ala Ser Thr Thr Val Pro Lys Met Leu Val
1                                5                                10                                15

Asn Ile Gln Ala Gln Ser Lys Val Ile Thr Tyr Ala Gly Cys Ile Thr
                                20                                25                                30

Gln Met Tyr Phe Phe Thr His Phe Val Gly Leu Asp Ser Phe Leu Leu
                                35                                40                                45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50                                55                                60

Tyr Thr Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Ala
65                                70                                75                                80

Ser Trp Ile Met Ser Val Leu His Ser Leu Leu Gln Ser Leu Met Val
                                85                                90                                95

Leu Arg Leu Ser Leu Cys Arg Glu Leu Glu Ile Pro His Phe Phe Cys
                                100                                105                                110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Ser Asp Thr Phe Leu Asp
115                                120                                125

Asp Met Val Met Tyr Leu Ala Ala Val Leu Leu Gly Gly Gly Cys Leu
130                                135                                140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Cys Ala
145                                150                                155                                160

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Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Ser Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Ile His Asn Ser His Ser Ser Ala Ile Ala Ser
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 126
<211> 649
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO27; Accession DDBJ/EMBL/GenBank = AF127897

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 126
c ctg gtt gat ttc tgt ctg gcc acc gac acc atc ccc aag atg ctg gtg 49
Leu Val Asp Phe Cys Leu Ala Thr Asp Thr Ile Pro Lys Met Leu Val
1 5 10 15
agc ctt caa acc agg agc aag gcc atc tct tat ccc tgc tgc ctg acc 97
Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
20 25 30
cag atg tac ttc ttc cat ttc ttt ggc atc gtg gac agc gtc tta att 145
Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Val Leu Ile
35 40 45
gct gta atg gcg tat gac cgc ttt gtg gcc atc tgc cac ccc ttg cac 193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60
tac gcc acg atc atg agc cca cgc ctc tgt ggc ctg ctg gtc ggg gcc 241
Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala
65 70 75 80
ccc tgg gtg ttt tca tgc ttc atc tca ctc acc cac atc ctc ctg atg 289
Pro Trp Val Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
85 90 95
gcc cgc ctc gtt ttc tgc ggc agc ctc aag gtg cct cat tac ttg tgc 337
Ala Arg Leu Val Phe Cys Gly Ser Leu Lys Val Pro His Tyr Leu Cys
100 105 110
gac ctc act ccc atc ctc cga ctt tcg tgc aca gac acg tct gtg aac 385
Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
115 120 125
agg att ttc atc ctc act gtg gca ggg atg gtg ata gcc acg ccc ttc 433
Arg Ile Phe Ile Leu Thr Val Ala Gly Met Val Ile Ala Thr Pro Phe

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130              135              140
atc tgc atc ctg gcc tcc tat gct tgc atc ctt gta gcc atc atg aag      481
Ile Cys Ile Leu Ala Ser Tyr Ala Cys Ile Leu Val Ala Ile Met Lys
145              150              155              160

atc ccc tct gca ggt ggc agg aag aaa gcc ttc tcc acc tgc agc tcc      529
Ile Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
165              170              175

cac ctg tcc gtg gtt gct ctc ttc tat ggg acc acc att ggg gtc tac      577
His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180              185              190

ctg tgt ccc tcc tcg gtc cac acc gct gta aag gag aaa gct tct gct      625
Leu Cys Pro Ser Ser Val His Thr Ala Val Lys Glu Lys Ala Ser Ala
195              200              205

gtg atg tac aca gta gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro      649
210              215

<210> 127
<211> 216
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO27; Accession DDBJ/EMBL/GenBank = AF127897

<400> 127
Leu Val Asp Phe Cys Leu Ala Thr Asp Thr Ile Pro Lys Met Leu Val
1              5              10              15

Ser Leu Gln Thr Arg Ser Lys Ala Ile Ser Tyr Pro Cys Cys Leu Thr
20              25              30

Gln Met Tyr Phe Phe His Phe Phe Gly Ile Val Asp Ser Val Leu Ile
35              40              45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50              55              60

Tyr Ala Thr Ile Met Ser Pro Arg Leu Cys Gly Leu Leu Val Gly Ala
65              70              75              80

Pro Trp Val Phe Ser Cys Phe Ile Ser Leu Thr His Ile Leu Leu Met
85              90              95

Ala Arg Leu Val Phe Cys Gly Ser Leu Lys Val Pro His Tyr Leu Cys
100             105             110

Asp Leu Thr Pro Ile Leu Arg Leu Ser Cys Thr Asp Thr Ser Val Asn
115             120             125

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Arg Ile Phe Ile Leu Thr Val Ala Gly Met Val Ile Ala Thr Pro Phe
130 135 140

Ile Cys Ile Leu Ala Ser Tyr Ala Cys Ile Leu Val Ala Ile Met Lys
145 150 155 160

Ile Pro Ser Ala Gly Gly Arg Lys Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

His Leu Ser Val Val Ala Leu Phe Tyr Gly Thr Thr Ile Gly Val Tyr
180 185 190

Leu Cys Pro Ser Ser Val His Thr Ala Val Lys Glu Lys Ala Ser Ala
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 128
<211> 646
<212> DNA
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 27679; gene = SBO28; Accession DDBJ/EMBL/GenBank = AF127898

<220>
<221> CDS
<222> (2)..(646)
<223> Product = olfactory receptor

<400> 128
c ttg gct gac att ggt ttc acc tcc acc aca gtc ccc agg aca att gtg 49
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1 5 10 15

aac att caa act cac agc aga gtc atc gcc tat gcg agc tgc ctg aca 97
Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20 25 30

cag atg tct ttt tca ata ttt ttt gcg tgt atg gaa gac acg ctc ctg 145
Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
35 40 45

gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac 193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg 241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65 70 75 80

tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc 289
Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85 90 95

tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt 337
Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys

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gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat      385
Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
      115                      120                      125

aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc      433
Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
      130                      135                      140

tca ggg atc ttt ttc tct tac tat aaa att gcc ccc tcc att ctg aga      481
Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Pro Ser Ile Leu Arg
      145                      150                      155

gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct      529
Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
      165                      170                      175

cac ctg gca gtt gtt tgc tta ttt tat gga aca gtc att gga gtg tac      577
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
      180                      185                      190

ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg      625
Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
      195                      200                      205

atg tac aca gtg gtc act ccc      646
Met Tyr Thr Val Val Thr Pro
      210                      215

<210> 129
<211> 215
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 27679; gene = SBO28; Accession DDBJ/EMBL/GenBank = AF127898

<400> 129
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1          5          10          15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
20          25          30

Gln Met Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
35          40          45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50          55          60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65          70          75          80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
85          90          95

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Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
 100 105 110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
 115 120 125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
 130 135 140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Pro Ser Ile Leu Arg
 145 150 155 160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
 180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
 195 200 205

Met Tyr Thr Val Val Thr Pro
 210 215

<210> 130
 <211> 649
 <212> DNA
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 27679; gene = SBO29; Accession DDBJ/EMBL/GenBank = AF127899
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 130
 c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15
 aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30
 cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45
 act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala

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65              70              75              80
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg      289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
              85              90              95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cgc ttt ttc tgc      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
              100              105              110

gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat      385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
              115              120              125

gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc      433
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
              130              135              140

aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca      481
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
              145              150              155              160

atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
              165              170              175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac      577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
              180              185              190

ctt agt tct gct gca act ggc aac tca cat tca ggt gct gca gcc ttg      625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Leu
              195              200              205

gtg atg tac act gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro      649
              210              215

<210> 131
<211> 216
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO29; Accession DDBJ/EMBL/GenBank = AF127899

<400> 131
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1              5              10              15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
              20              25              30

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
              35              40              45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
50              55              60

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Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro Arg Phe Phe Cys
100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Gly Ala Ala Ala Leu
195 200 205

Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 132

<211> 649

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor

<400> 132

c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca gac tgc atc acc 97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
20 25 30

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg 145
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu

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          35              40              45
act gtg atg gcc tat gac cgg tat gtg gcc acc tgt cac ccc ctg cac      193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His
  50              55              60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca      241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
  65              70              75              80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg      289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
              85              90              95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc      337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
              100              105              110

gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat      385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
              115              120              125

gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc      433
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
              130              135              140

aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca      481
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
              145              150              155              160

atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
              165              170              175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac      577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
              180              185              190

ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg      625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
              195              200              205

gtg atg tac aca gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro      649
  210              215

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<210> 133
<211> 216
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO30; Accession DDBJ/EMBL/GenBank = AF127900

<400> 133
Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
1              5              10              15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Asp Cys Ile Thr
              20              25              30

```

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Thr Cys His Pro Leu His
 50 55 60
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
 85 90 95
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110
 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
 115 120 125
 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
 130 135 140
 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr
 180 185 190
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 134
 <211> 649
 <212> DNA
 <213> Saimiri sciureus

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901

 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

 <400> 134
 c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val

09747155-030901

1	5	10	15	
aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc				97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr	20	25	30	
cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg				145
Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu	35	40	45	
act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac				193
Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His	50	55	60	
tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca				241
Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala	65	70	75	80
tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa acc tta ata gtg				289
Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Thr Leu Ile Val	85	90	95	
ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc				337
Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys	100	105	110	
gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat				385
Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn	115	120	125	
gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc				433
Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu	130	135	140	
aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca				481
Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala	145	150	155	160
atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct				529
Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser	165	170	175	
cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gtg tac				577
His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Val Tyr	180	185	190	
ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg				625
Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu	195	200	205	
gtg atg cac aca gtg gtc acc ccc				649
Val Met His Thr Val Val Thr Pro	210	215		

<210> 135
 <211> 216
 <212> PRT
 <213> Saimiri sciureus

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9521; gene = SSC31; Accession DDBJ/EMBL/GenBank = AF127901

 <400> 135


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<220>
<221> CDS
<222> (2)..(646)
<223> Product = olfactory receptor

<400> 136
c ttg gct gac att ggt ttc acc tcc acc aca gtc ccc agg aca att gtg      49
  Leu Ala Asp Ile Gly Phe Thr Ser Thr Val Pro Arg Thr Ile Val
    1          5          10          15

aac att caa act cac agc aga gtc atc gcc tat gcg agc tgc ctg aca      97
Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
          20          25          30

cag gtg tct ttt tca atc ttt ttt gcg tgt atg gaa gac acg ctc ctg      145
Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
          35          40          45

gct gtg atg gcc tat gac cgg ttt gtt gcc atc tgt cac ccc ctg cac      193
Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50          55          60

tac cca gtc atc atg aac cca cga ctc tgt ggc ttc tta gtg ttg gtg      241
Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
          65          70          75          80

tct gtt ttt ctt agc ctt tta ata tcc cag gtg cac aat ttg att gtc      289
Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
          85          90          95

tta caa ttt tct tgc ttc aaa gag ata aag att tct aat ttc ttc tgt      337
Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
          100          105          110

gac cct tct caa ctc ctc acc ctt tct tgt tct gac acc ttt gtc aat      385
Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
          115          120          125

aac ata gtc acg aat ttc ttt gct gct gta ttt ggt ttt ctt ccc atc      433
Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
          130          135          140

tca ggg atc ttt ttc tct tac tat aaa att gcc tcc tcc att ctg aga      481
Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg
          145          150          155          160

gtt cca tta tca agt ggg aag tat aaa gcc ttc tcc acc tgt agc tct      529
Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
          165          170          175

cac ctg gca gtt gtt tgc tta ttt tat gga aca gtt att gga gtg tac      577
His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
          180          185          190

ctt ggg tca tca atg gca tcc ccc agg aag agt gtg gtg gcc tca gtg      625
Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
          195          200          205

atg tac aca gtg gtc act ccc      646
Met Tyr Thr Val Val Thr Pro
          210          215

<210> 137
<211> 215
<212> PRT

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<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(646)
<223> Taxon = 9521; gene = SSC32; Accession DDBJ/EMBL/GenBank = AF127902

<400> 137
Leu Ala Asp Ile Gly Phe Thr Ser Thr Thr Val Pro Arg Thr Ile Val
1          5          10          15

Asn Ile Gln Thr His Ser Arg Val Ile Ala Tyr Ala Ser Cys Leu Thr
          20          25          30

Gln Val Ser Phe Ser Ile Phe Phe Ala Cys Met Glu Asp Thr Leu Leu
          35          40          45

Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
          50          55          60

Tyr Pro Val Ile Met Asn Pro Arg Leu Cys Gly Phe Leu Val Leu Val
65          70          75          80

Ser Val Phe Leu Ser Leu Leu Ile Ser Gln Val His Asn Leu Ile Val
          85          90          95

Leu Gln Phe Ser Cys Phe Lys Glu Ile Lys Ile Ser Asn Phe Phe Cys
          100          105          110

Asp Pro Ser Gln Leu Leu Thr Leu Ser Cys Ser Asp Thr Phe Val Asn
          115          120          125

Asn Ile Val Thr Asn Phe Phe Ala Ala Val Phe Gly Phe Leu Pro Ile
          130          135          140

Ser Gly Ile Phe Phe Ser Tyr Tyr Lys Ile Ala Ser Ser Ile Leu Arg
145          150          155          160

Val Pro Leu Ser Ser Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ser Ser
          165          170          175

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
          180          185          190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
          195          200          205

Met Tyr Thr Val Val Thr Pro
          210          215

<210> 138
<211> 649

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<212> DNA
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 9521; gene = SSC33; Accession DDBJ/EMBL/GenBank = AF127903

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 138
c ttc tct gac ctc tgc ttc tct tct gtg acc att cca aag ttg tta cag      49
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
 1             5             10             15

aac atg cag agc caa gac cca tcc atc ccc tat gcg ggc tgc ctg acc      97
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
      20             25             30

cag atg tac ttc ttc ttg tat ttt tcg gat cta gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
      35             40             45

gtg gcc atg gcc tat gac cgc tac gtg gcc atc tgc ctc ccc cta cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu His
      50             55             60

tac gcc acc atc atg agc ccc atg ctg tct cgc tcc ctg gtg gcg ctg      241
Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
      65             70             75

tcc tgg gtg ctg acc acc ttc cat gcc atg ttg cac act tta ctc atg      289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
      85             90             95

gcc agg ttg cgt ttt tgt gca gac aat gtg atc ctc cac ttt ttc tgt      337
Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
      100            105            110

gat atg tct gct ctg ctg aag ctg gcc tgc tct gac act cga gtt aat      385
Asp Met Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Thr Arg Val Asn
      115            120            125

gaa ttg gtg ata ttt atc atg gga ggc ctc att ctt gtc atc cca ctt      433
Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
      130            135            140

cta ctt atc att ggg tcc tac gca cga att gtc ttc tcc atc ctc aag      481
Leu Leu Ile Ile Gly Ser Tyr Ala Arg Ile Val Phe Ser Ile Leu Lys
      145            150            155            160

gtc cct tct tct aag ggt atc tgc aag gcc gtc tct act tgt ggc tcc      529
Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
      165            170            175

cac ctc tct gtg gtg tca ctg ttc tat ggg act gtt att ggt ctc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Val Ile Gly Leu Tyr
      180            185            190

tta tgc cca tca gct aat aat tct act cta aag gag act gtc atg gct      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
      195            200            205

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649

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<400> 139
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
1          5          10          15
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Gln Met Tyr Phe Phe Leu Tyr Phe Ser Asp Leu Glu Ser Phe Leu Leu
35 40 45

Tyr Ala Thr Ile Met Ser Pro Met Leu Ser Arg Ser Leu Val Ala Leu
65 70 75 80

Ala Arg Leu Arg Phe Cys Ala Asp Asn Val Ile Leu His Phe Phe Cys
100 105 110

Glu Leu Val Ile Phe Ile Met Gly Gly Leu Ile Leu Val Ile Pro Leu
130 135 140

Val Pro Ser Ser Lys Gly Ile Cys Lys Ala Val Ser Thr Cys Gly Ser
165 170 175

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Glu Thr Val Met Ala
195 200 205

Variable	Mean	Standard Deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	0.5	0.5	0	1
Marital Status	0.5	0.5	0	1
Education	12.5	1.5	10	15
Income	35000	15000	10000	60000
Health	0.5	0.5	0	1
Smoking	0.2	0.4	0	1
Drinking	0.1	0.3	0	1
Exercise	0.3	0.5	0	1
Stress	0.4	0.5	0	1
Sleep	0.5	0.5	0	1
Work	0.5	0.5	0	1
Family	0.5	0.5	0	1
Friends	0.5	0.5	0	1
Hobbies	0.5	0.5	0	1
Travel	0.5	0.5	0	1
Volunteering	0.5	0.5	0	1
Religion	0.5	0.5	0	1
Politics	0.5	0.5	0	1
Art	0.5	0.5	0	1
Music	0.5	0.5	0	1
Gardening	0.5	0.5	0	1
Cooking	0.5	0.5	0	1
Reading	0.5	0.5	0	1
Writing	0.5	0.5	0	1
Learning	0.5	0.5	0	1
Teaching	0.5	0.5	0	1
Managing	0.5	0.5	0	1
Organizing	0.5	0.5	0	1
Planning	0.5	0.5	0	1
Decision Making	0.5	0.5	0	1
Problem Solving	0.5	0.5	0	1
Communication	0.5	0.5	0	1
Interpersonal Skills	0.5	0.5	0	1
Leadership	0.5	0.5	0	1
Teamwork	0.5	0.5	0	1
Conflict Resolution	0.5	0.5	0	1
Emotional Stability	0.5	0.5	0	1
Resilience	0.5	0.5	0	1
Adaptability	0.5	0.5	0	1
Flexibility	0.5	0.5	0	1
Openness	0.5	0.5	0	1
Conscientiousness	0.5	0.5	0	1
Neuroticism	0.5	0.5	0	1
Agreeableness	0.5	0.5	0	1
Extraversion	0.5	0.5	0	1
Introversion	0.5	0.5	0	1
Optimism	0.5	0.5	0	1
Pessimism	0.5	0.5	0	1
Self-Esteem	0.5	0.5	0	1
Self-Confidence	0.5	0.5	0	1
Self-Motivation	0.5	0.5	0	1
Self-Discipline	0.5	0.5	0	1
Self-Regulation	0.5	0.5	0	1
Self-Improvement	0.5	0.5	0	1
Self-Reflection	0.5	0.5	0	1
Self-Analysis	0.5	0.5	0	1
Self-Criticism	0.5	0.5	0	1
Self-Compassion	0.5	0.5	0	1
Self-Understanding	0.5	0.5	0	1
Self-Awareness	0.5	0.5	0	1
Self-Insight	0.5	0.5	0	1
Self-Discovery	0.5	0.5	0	1
Self-Exploration	0.5	0.5	0	1
Self-Expression	0.5	0.5	0	1
Self-Realization	0.5	0.5	0	1
Self-Fulfillment	0.5	0.5	0	1
Self-Actualization	0.5	0.5	0	1
Self-Transcendence	0.5	0.5	0	1
Self-Enlightenment	0.5	0.5	0	1
Self-Mastery	0.5	0.5	0	1
Self-Perfection	0.5	0.5	0	1
Self-Perseverance	0.5	0.5	0	1
Self-Persistence	0.5	0.5	0	1
Self-Endurance	0.5	0.5	0	1
Self-Strength	0.5	0.5	0	1
Self-Power	0.5	0.5	0	1
Self-Force	0.5	0.5	0	1
Self-Will	0.5	0.5	0	1
Self-Determination	0.5	0.5	0	1
Self-Choice	0.5	0.5	0	1
Self-Action	0.5	0.5	0	1
Self-Initiative	0.5	0.5	0	1
Self-Responsibility	0.5	0.5	0	1
Self-Accountability				

His Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Val Ile Gly Val Tyr
180 185 190

Leu Gly Ser Ser Met Ala Ser Pro Arg Lys Ser Val Val Ala Ser Val
195 200 205

Met Tyr Thr Val Val Thr Pro
210 215

<210> 142
<211> 649
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO64; pseudogene; Accession DDBJ/EMBL/GenBank
= AF127905

<400> 142
ctttgtcgat ttctgttatt ccaccaccgt tatacccaaa ctgctggaga acttggttgt 60
ggaagacaga agcatctcct tcacaggatg cgtcatgcaa ttcttttttg ccagcatatt 120
tgtggtgaca gaaatattca tgctggcagt gatggcctat gacagatttg tgggtggtgtg 180
ttaccctctg ctctacacag ttgcaatgtc ccagaggcct ttcttttttg tagtggctac 240
atcatacttc agggtgacag tctgtttctt gacaattacc ttctttctcc tggaattatc 300
cttcagagga aataatatca ttaataactt tgtgtgtgag cctgctgcca ttgttgctgt 360
gccatgcttt gaccctaca tgagccagga aatcattttc atttctgcca cattcaatga 420
aacaagcagc ctgatgatca ttctcacctc ctaagatttc gtttttatca atgtcatgat 480
gatgccttcc actggggggc gcataaaagc atgcgcgacc tgttcctccc agctgaccgc 540
cattatcatt ttccatggga ccattctttt tctctattgt gttcctaact ccaaaagttc 600
atgggtcatg gtcaagggtg gctctatctt ttacacagtg gtcaccccc 649

<210> 143
<211> 649
<212> DNA
<213> Saimiri boliviensis
<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor

<400> 143
c ttt gta gac atc tgt gtt acc tcc acc acg att cca aag aca cta tca 49

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Phe Val Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Thr Leu Ser
1           5           10           15

aac atc cag aca cac agc aaa gtc atc acc tat gca ggc tgt gtc acc      97
Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
           20           25           30

cag ttg tac ttt tct gta ctc ttt ata ggg ttg gac agc tta ctc ctg      145
Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu
           35           40           45

acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctg cgc      193
Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
           50           55           60

tac atg gtc atc atg aac cct cag ctc tgt gga ctg ctg gtt ctg gtg      241
Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val
           65           70           75

tcc tgg atc atg agt gcc ctg cat tcc ttg aca gaa agc tta atg gca      289
Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala
           85           90           95

tta tca ctg ctc ttt tgt aca gac ttg aaa atc ctc cac ttt ttc tgt      337
Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Phe Cys
           100          105          110

gaa ctt aat cag ata atc cac att gcc tgt tct gac acc tgt ctt aat      385
Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn
           115          120          125

aac ctg gtg atg tat ttg tca gct gtg ctg ctg ggc ggt ggt cct ctc      433
Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu
           130          135          140

gct ggg atc ctg tac tct tac tct aag ata gct tcc tct ata cgt gca      481
Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
           145          150          155

atc tca tca gct aag ggg aag tac aag gca ttt tcc acc tgt gca tct      529
Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
           165          170          175

cac ctc tca gtt gtc tcc tta ttt tat tgt aca ggc cta ggg gtg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
           180          185          190

ctg agt tct gct gca acc cac aac tca ctc tca agt aca gca gcc tcg      625
Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser
           195          200          205

gtg atg tac act gtg gtc acc ccc
Val Met Tyr Thr Val Val Thr Pro
           210          215

<210> 144
<211> 216
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 27679; gene = SBO65; Accession DDBJ/EMBL/GenBank = AF127906

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<400> 144
 Phe Val Asp Ile Cys Val Thr Ser Thr Thr Ile Pro Lys Thr Leu Ser
 1 5 10 15
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Tyr Ala Gly Cys Val Thr
 20 25 30
 Gln Leu Tyr Phe Ser Val Leu Phe Ile Gly Leu Asp Ser Leu Leu Leu
 35 40 45
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu Arg
 50 55 60
 Tyr Met Val Ile Met Asn Pro Gln Leu Cys Gly Leu Leu Val Leu Val
 65 70 75 80
 Ser Trp Ile Met Ser Ala Leu His Ser Leu Thr Glu Ser Leu Met Ala
 85 90 95
 Leu Ser Leu Leu Phe Cys Thr Asp Leu Lys Ile Leu His Phe Phe Cys
 100 105 110
 Glu Leu Asn Gln Ile Ile His Ile Ala Cys Ser Asp Thr Cys Leu Asn
 115 120 125
 Asn Leu Val Met Tyr Leu Ser Ala Val Leu Leu Gly Gly Gly Pro Leu
 130 135 140
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Ala Ser Ser Ile Arg Ala
 145 150 155 160
 Ile Ser Ser Ala Lys Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Cys Thr Gly Leu Gly Val Tyr
 180 185 190
 Leu Ser Ser Ala Ala Thr His Asn Ser Leu Ser Ser Thr Ala Ala Ser
 195 200 205
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 145
 <211> 649
 <212> DNA
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor

<400> 145
 c ttt gta gac atc tgt ttt gtg tct acc act gtc ccg aag atg ctg gta 49
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

aat atc cag aca cac agc aaa gtc atc acc ttt gca ggc tgc atc acc 97
 Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

cag ata ggc cat tgc cta ctc ttt gca gca ttg gac atc ttt atg ctg 145
 Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45

act gtg atg gcc tat gac cgg tat gtg gcc atc tgt cac ccc ctg cac 193
 Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca gtc acc att aac ccc aga ctg tgt gga ctg ctg gtt ctg gca 241
 Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

tcc tgg atc ctg agt gcc ctg aat tcc tca tta caa ccc tta ata gtg 289
 Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
 85 90 95

ctg cgg ctt tcc ttc tgc aca gac ttg gaa atc ccc cac ttt ttc tgc 337
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

gaa ctt aat cag gtc ata cat ctt gcc tgt tat gac act ttc ctt aat 385
 Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
 115 120 125

gat gtg gtg atg tat ttg gca gct atg ctg ctg ggc ggt ggt ccc ctc 433
 Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Pro Leu
 130 135 140

aca gga att att tac tct tac tct aag ata gtt tcc tcc ata cgt gca 481
 Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

atc tca tca gct cag ggg aag tac aag gcg ttt tcc acc tgt gca tct 529
 Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

cac atc tta att gtc tcc tta ttt tat ggt aca ctc cta ggt gcg tac 577
 His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr
 180 185 190

ctt agt tct gct gca act ggc aac tca cat tca agt gct gca gcc ttg 625
 Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205

gtg atg tac act gtg gtc acc ccc 649
 Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 146
 <211> 216

<212> PRT
 <213> Saimiri sciureus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 9521; gene = SSC69; Accession DDBJ/EMBL/GenBank = AF127907

<400> 146
 Phe Val Asp Ile Cys Phe Val Ser Thr Thr Val Pro Lys Met Leu Val
 1 5 10 15

Asn Ile Gln Thr His Ser Lys Val Ile Thr Phe Ala Gly Cys Ile Thr
 20 25 30

Gln Ile Gly His Cys Leu Leu Phe Ala Ala Leu Asp Ile Phe Met Leu
 35 40 45

Thr Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60

Tyr Thr Val Thr Ile Asn Pro Arg Leu Cys Gly Leu Leu Val Leu Ala
 65 70 75 80

Ser Trp Ile Leu Ser Ala Leu Asn Ser Ser Leu Gln Pro Leu Ile Val
 85 90 95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Glu Ile Pro His Phe Phe Cys
 100 105 110

Glu Leu Asn Gln Val Ile His Leu Ala Cys Tyr Asp Thr Phe Leu Asn
 115 120 125

Asp Val Val Met Tyr Leu Ala Ala Met Leu Leu Gly Gly Gly Pro Leu
 130 135 140

Thr Gly Ile Ile Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160

Ile Ser Ser Ala Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Ala Ser
 165 170 175

His Ile Leu Ile Val Ser Leu Phe Tyr Gly Thr Leu Leu Gly Ala Tyr
 180 185 190

Leu Ser Ser Ala Ala Thr Gly Asn Ser His Ser Ser Ala Ala Ala Leu
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 147

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<211> 487
<212> DNA
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA133; Accession DDBJ/EMBL/GenBank = AF179716

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 147
t  gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
   Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
   1              5              10              15

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
              20              25              30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
              35              40              45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
              50              55              60

gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
              65              70              75              80

ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
              85              90              95

cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
              100              105              110

aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
              115              120              125

tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
              130              135              140

act cta aag gag act gtt atg gct atg atg tac act gtg gtg acc ccc      481
Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
              145              150              155              160

atg ctg
Met Leu
                                         487

<210> 148
<211> 162
<212> PRT
<213> Papio hamadryas

<220>

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<221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9557; gene = PPA133; Accession DDBJ/EMBL/GenBank = AF179716

<400> 148
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
 130 135 140

Thr Leu Lys Glu Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 149
 <211> 486
 <212> DNA
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9557; gene = PPA134; Accession DDBJ/EMBL/GenBank = AF179717

<220>
 <221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor

<400> 149
 t gtt gcc atc tgc cag cct ctg cac tac tct acc ctc ttg agc cca tgg 49

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Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
1           5           10           15

gcc tgc atg gcc atg gtg ggc acc tcc tgg ctc aca ggc atc atc acg      97
Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
                20                25                30

gcc acc acc cat gcc ttc ctc atc ttc tct cta cct ttt ccc agc cgc      145
Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
                35                40                45

cca atc atc cca cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg      193
Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
                50                55                60

gca agt gct ggg aag cac agg agc gag atc tct gtg atg aca gcc act      241
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
                65                70                75                80

gta gtc ttc att atg atc ccc ttc tct ctg att gtc acc tct tac atc      289
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
                85                90                95

cgc atc ctg gga gcc atc cta gcg atg gcc tcc acc cag agc cgc cgc      337
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
                100                105                110

aag gtc ttc tcc acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc      385
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
                115                120                125

ttt gga aca gcc agc atc acc tac atc cgg ccg cag gca ggc tcc tct      433
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
                130                135                140

gtt acc aca gac cgc gtc ctc agt gtg ttc tac acg gtc atc aca ccc      481
Val Thr Thr Asp Arg Val Leu Ser Val Phe Tyr Thr Val Ile Thr Pro
                145                150                155                160

atg ct
Met
210
211
212
213
220
221
222
223
400
Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
1           5           10           15

Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
                20                25                30

Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
                35                40                45

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<212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(482)
 <223> Taxon = 9557; gene = PPA136; pseudogene; Accession DDBJ/EMBL/Genbank = 179719

<400> 152
 tgtggccatc tgccaccccc tctactatgt cacagccatg agtcctggac tctgtatctt 60
 gctcctctgc ttgtgttggg ggctctctgt tctctatggg ctctctctca ctctcctcct 120
 gaccagggtg accttctgtg ggactcaaga gatccactac ctcttctgtg agatgtacgt 180
 cctgctgcag ctggcatgtt ccaacaccca catcattcac acagtgtctg ttgctactgg 240
 ctgctttctt cctcgacccc ttagggttca cgaactacatc ctatatacgt attgtcagaa 300
 ccatccttca gataccctca gcctctaaga aacacaaaac cttctctgcc tgtgcctcac 360
 atttgggtgt ggtctccctc ttttatggga cacttggtat ggtatacctg cagcccctcc 420
 acacctaact catgaaggac tcagtagcca cagtgatgta tgctgtgggtg acacctatga 480
 tg 482

<210> 153
 <211> 481
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(481)
 <223> Taxon = 9557; gene = PPA137; Accession DDBJ/EMBL/GenBank = AF179720
 <220>
 <221> CDS
 <222> (2)..(481)
 <223> Product = olfactory receptor

<400> 153
 c ctg gca ata tgt caa ccc ctg cgc tac cca gtg ctc atg aat ggg agg 49
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
 1 5 10 15
 tta tgc aca gtc ctt gtg gct gga gct tgg gtc gcc ggc tcc att cat 97
 Leu Cys Thr Val Leu Val Ala Gly Ala Trp Val Ala Gly Ser Ile His
 20 25 30
 ggg tct atc cag gcc acc ctg acc ttc cgc cta ccc tat tgt ggg ccc 145
 Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
 35 40 45
 aat cag gta gat tac ttt atc tgt gac atc cct gca gta ttg aga ctg 193
 Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
 50 55 60
 gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac atc 241
 Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Ile
 65 70 75 80
 gga gta gtg gcc gcc agt tgc ttc atg tta att cta ctt tcc tat gcc 289

Leu Asp Gly Ala Val Ala Val Phe Tyr Thr Val Val Thr Pro Phe Leu
 145 150 155 160

<210> 155
 <211> 487
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9557; gene = PPA138; Accession DDBJ/EMBL/GenBank = AF179721
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 155
 t gta gcc ata tgc aaa cct tta ctt tat cca gtg att atg acc aat gga 49
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly
 1 5 10 15
 ctg tgc atc cgg cta tta gtc ttg tca ttt gta ggt ggc ttc ctt cat 97
 Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
 20 25 30
 gcc tta att cat gaa ggc att tta ttc aga tta acc ttc tgt aat tct 145
 Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
 35 40 45
 aac ata ata cat cac ttt tac tgt gac att atc cca ttg tta acg att 193
 Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
 50 55 60
 tcc tgt act gac cct tct att aat ttt tta atg ctt ttt att ttg tct 241
 Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
 65 70 75 80
 ggt tca ata cag gta ttc act att ttg act gtt ctt gtc tct tat gca 289
 Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
 85 90 95
 ttt gtc ctc ttt aca atc tta aaa aaa aag tca gtc aaa ggc ata agg 337
 Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg
 100 105 110
 aaa gcc ttt tcc acc tgt gga gcc cat ctc ttc tct gtc tgt tta tac 385
 Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
 115 120 125
 tat ggc ccc ctt ctc ttc atg tat gtg ggc cct gca tct cca caa gca 433
 Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
 130 135 140
 gat gat caa gat atg gta gag tgt gta ttt tac act gtc atc att cct 481
 Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
 145 150 155 160
 ttc tta 487
 Phe Leu

<210> 156

<211> 162
 <212> PRT
 <213> Papio hamadryas

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9557; gene = PPA138; Accession DDBJ/EMBL/GenBank = AF179721

<400> 156
 Val Ala Ile Cys Lys Pro Leu Leu Tyr Pro Val Ile Met Thr Asn Gly
 1 5 10 15

Leu Cys Ile Arg Leu Leu Val Leu Ser Phe Val Gly Gly Phe Leu His
 20 25 30

Ala Leu Ile His Glu Gly Ile Leu Phe Arg Leu Thr Phe Cys Asn Ser
 35 40 45

Asn Ile Ile His His Phe Tyr Cys Asp Ile Ile Pro Leu Leu Thr Ile
 50 55 60

Ser Cys Thr Asp Pro Ser Ile Asn Phe Leu Met Leu Phe Ile Leu Ser
 65 70 75 80

Gly Ser Ile Gln Val Phe Thr Ile Leu Thr Val Leu Val Ser Tyr Ala
 85 90 95

Phe Val Leu Phe Thr Ile Leu Lys Lys Lys Ser Val Lys Gly Ile Arg
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ala His Leu Phe Ser Val Cys Leu Tyr
 115 120 125

Tyr Gly Pro Leu Leu Phe Met Tyr Val Gly Pro Ala Ser Pro Gln Ala
 130 135 140

Asp Asp Gln Asp Met Val Glu Cys Val Phe Tyr Thr Val Ile Ile Pro
 145 150 155 160

Phe Leu

<210> 157
 <211> 487
 <212> DNA
 <213> Papio hamadryas

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722

<220>
 <221> CDS

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<222> (2)..(487)
<223> Product = olfactory receptor

<400> 157
t gtg gcc att tgt aac cct ctg ctc tac atg gtg gtg gtg tct cgg cgg      49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
1 5 10 15

ctc tgc ctc ctg ctg gtc tcc ctc aca tac ctc tat ggc ttt tct aca      97
Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
20 25 30

gct att gtg gtt tca cct tgt ata ttc tct atg tct tat tgc tct tct      145
Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
35 40 45

aat ata atc aat cat ttt tac tgt gat att gca cct ctg tta gca tta      193
Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
50 55 60

tct tgc tct gat act tac tta cca gaa gca ata gtc ttc ata tct gca      241
Ser Cys Ser Asp Thr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
65 70 75 80

gca aca aat ttg gtt ttt tcc atg att aca gtt cta gta tct tat ttc      289
Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
85 90 95

aat att gtt ttg tcc att cta agg atg cat tca tca gaa gga agg aaa      337
Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
100 105 110

aaa gcc ttt tcc acc tgt gct tca cat atg atg gca gtc aca gtt ttc      385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
115 120 125

tat ggg aca atg ctg ttc atg tat ttg cag ccc caa acc aac cac tca      433
Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
130 135 140

ctg gat act gat aag atg gct tct gtg ttt tac aca ttg gtg att cct      481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
145 150 155 160

atg ctg
Met Leu      487

<210> 158
<211> 162
<212> PRT
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA139; Accession DDBJ/EMBL/GenBank = AF179722

<400> 158
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Val Val Ser Arg Arg
1 5 10 15

Leu Cys Leu Leu Leu Val Ser Leu Thr Tyr Leu Tyr Gly Phe Ser Thr
20 25 30

```

Ala Ile Val Val Ser Pro Cys Ile Phe Ser Met Ser Tyr Cys Ser Ser
35 40 45

Asn Ile Ile Asn His Phe Tyr Cys Asp Ile Ala Pro Leu Leu Ala Leu
50 55 60

Ser Cys Ser Asp Thr Tyr Leu Pro Glu Ala Ile Val Phe Ile Ser Ala
65 70 75 80

Ala Thr Asn Leu Val Phe Ser Met Ile Thr Val Leu Val Ser Tyr Phe
85 90 95

Asn Ile Val Leu Ser Ile Leu Arg Met His Ser Ser Glu Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Met Met Ala Val Thr Val Phe
115 120 125

Tyr Gly Thr Met Leu Phe Met Tyr Leu Gln Pro Gln Thr Asn His Ser
130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Val Ile Pro
145 150 155 160

Met Leu

<210> 159
<211> 487
<212> DNA
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF179723

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 159
t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1 5 10 15

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97
Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgc gca gac 145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35 40 45

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aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50                               55                               60

gcc tgc tct gac act cga gtc aat gaa ttg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
 65                               70                               75                               80

ggg ctg att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                        85                               90                               95

cgg att gtc tcc tcc atc ctc aag gtc cct tcg tct aag ggt atc tgc      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
                        100                               105                               110

aag gcg ttc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
      115                               120                               125

tat ggg acc att att ggt ctc tac ttc tgc cca tca gct aat agt tct      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
      130                               135                               140

act cta aag gag act gtt atg ggt atg atg tac act gtg gtg acc ccc      481
Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro
      145                               150                               155                               160

atg ctg      487
Met Leu

<210> 160
<211> 162
<212> PRT
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA140; Accession DDBJ/EMBL/GenBank = AF179723

<400> 160
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1                               5                               10                               15

Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
                20                               25                               30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35                               40                               45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50                               55                               60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65                               70                               75                               80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
                        85                               90                               95

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Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Cys Pro Ser Ala Asn Ser Ser
 130 135 140

Thr Leu Lys Glu Thr Val Met Gly Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 161
 <211> 478
 <212> DNA
 <213> Papio hamadryas
 <220>
 <221> misc_feature
 <222> (1)..(478)
 <223> Taxon = 9557; gene = PPA142; Accession DDBJ/EMBL/GenBank = AF179724

<220>
 <221> CDS
 <222> (2)..(478)
 <223> Product = olfactory receptor

<400> 161
 t gtg gcc atc tgt aag ccc ttg aac tat gca acc atc atg agt caa cct 49
 Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro
 1 5 10 15
 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat 97
 Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
 20 25 30
 gga ggg atc cag act ctg ttc ata gcc cag tta cca ttc tgt ggc ccc 145
 Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
 35 40 45
 aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg 193
 Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 50 55 60
 gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt 241
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 65 70 75 80
 gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc 289
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 85 90 95
 atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa 337
 Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
 100 105 110

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gct ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt      385
Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
      115                      120                      125

gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ccc act      433
Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
      130                      135                      140

gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg      478
Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
      145                      150                      155

<210> 162
<211> 159
<212> PRT
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(478)
<223> Taxon = 9557; gene = PPA142; Accession DDBJ/EMBL/GenBank = AF179724

<400> 162
Val Ala Ile Cys Lys Pro Leu Asn Tyr Ala Thr Ile Met Ser Gln Pro
1                      5                      10                      15

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
      20                      25                      30

Gly Gly Ile Gln Thr Leu Phe Ile Ala Gln Leu Pro Phe Cys Gly Pro
      35                      40                      45

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
      50                      55                      60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
65                      70                      75                      80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
      85                      90                      95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
      100                      105                      110

Ala Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
      115                      120                      125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Pro Thr
      130                      135                      140

Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
      145                      150                      155

<210> 163
<211> 487

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<212> DNA
<213> Papio hamadryas

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9557; gene = PPA143; Accession DDBJ/EMBL/GenBank = AF179725

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 163
t gtg gcc atc tgc aag cct ctg cat tac ttg aat atc atg aat cga aga      49
  Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
    1             5             10             15

gtc tgc aca ctg ctt gtt ttt act tct tgg ctg gtt tca ttc tta atc      97
Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
    20             25             30

ata ttc cca gca ctc atg ttg ctc tta cag ctt gat tac tgt agg tct      145
Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
    35             40             45

aat att atg gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt      193
Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
    50             55             60

gct tgt tca gac aca aaa ttc cta gag gtg atg gga ttt tct tgt gct      241
Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
    65             70             75             80

gtg ttt act cta atg ttg act ttg gca tta ata ttt ctg tcc tac ata      289
Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
    85             90             95

tac att atc aga aca att ttg aga att cct tct gct agt caa agg aca      337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
   100             105             110

aag gcc ttt tcc aca tgt tct tcc cac atg att gtc atc tcc atc tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
   115             120             125

tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
   130             135             140

gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc      481
Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
   145             150             155             160

atg ctg      487
Met Leu

<210> 164
<211> 162
<212> PRT
<213> Papio hamadryas

<220>
<221> misc_feature

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<222> (1)..(487)
 <223> Taxon = 9557; gene = PPA143; Accession DDBJ/EMBL/GenBank = AF179725

<400> 164
 Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
 1 5 10 15

Val Cys Thr Leu Leu Val Phe Thr Ser Trp Leu Val Ser Phe Leu Ile
 20 25 30

Ile Phe Pro Ala Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Arg Ser
 35 40 45

Asn Ile Met Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Gly Phe Ser Cys Ala
 65 70 75 80

Val Phe Thr Leu Met Leu Thr Leu Ala Leu Ile Phe Leu Ser Tyr Ile
 85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Thr
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
 130 135 140

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
 145 150 155 160

Met Leu

<210> 165
 <211> 487
 <212> DNA
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9557; gene = PPA144; Accession DDBJ/EMBL/GenBank = AF179726

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 165
 t gtt gcc atc tgc cag cct ctg cac tac tct acc ctc ttg agc cca tgg 49
 Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp

1	5	10	15	
gcc tgc atg gcc atg gtg ggc acc tcc tgg ctc aca ggc atc atc acg				97
Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr	20	25	30	
gcc acc acc cat gcc ttc ctc atc ttc tct cta cct ttt ccc agc cgc				145
Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg	35	40	45	
cca atc atc cca cac ttt ctc tgt gac atc ctg cca gta ctg agg ctg				193
Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu	50	55	60	
gca agt gct ggg aag cac agg agc gag atc tct gtg atg aca gcc act				241
Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr	65	70	80	
gta gtc ttc att atg atc ccc ttc tct ctg att gtc acc tct tac atc				289
Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile	85	90	95	
cgc atc ctg gga gcc atc cta gcg atg gcc tcc acc cag agc cgc cgc				337
Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg	100	105	110	
aag gtc ttc tcc acc tgc tcc tcc cat ctg ctc gtg gtc tct ctc ttc				385
Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe	115	120	125	
ttt gga aca gcc agc atc acc tac atc cgg ccg cag gca ggc tcc tct				433
Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser	130	135	140	
gtt acc aca gac cgc gtc ctc agt ctc ttc tac acg gtc atc aca ccc				481
Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro	145	150	155	160
atg ctc				487
Met Leu				

<210> 166
 <211> 162
 <212> PRT
 <213> Papio hamadryas

<220>
 <221> misc_feature
 <222> (1)..(487) <223> Taxon = 9557; gene = PPA144; Accession
 DDBJ/EMBL/GenBank = AF179726

<400> 166
 Val Ala Ile Cys Gln Pro Leu His Tyr Ser Thr Leu Leu Ser Pro Trp
 1 5 10 15

Ala Cys Met Ala Met Val Gly Thr Ser Trp Leu Thr Gly Ile Ile Thr
 20 25 30

Ala Thr Thr His Ala Phe Leu Ile Phe Ser Leu Pro Phe Pro Ser Arg
 35 40 45

Pro Ile Ile Pro His Phe Leu Cys Asp Ile Leu Pro Val Leu Arg Leu
50 55 60

Ala Ser Ala Gly Lys His Arg Ser Glu Ile Ser Val Met Thr Ala Thr
65 70 75 80

Val Val Phe Ile Met Ile Pro Phe Ser Leu Ile Val Thr Ser Tyr Ile
85 90 95

Arg Ile Leu Gly Ala Ile Leu Ala Met Ala Ser Thr Gln Ser Arg Arg
100 105 110

Lys Val Phe Ser Thr Cys Ser Ser His Leu Leu Val Val Ser Leu Phe
115 120 125

Phe Gly Thr Ala Ser Ile Thr Tyr Ile Arg Pro Gln Ala Gly Ser Ser
130 135 140

Val Thr Thr Asp Arg Val Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
145 150 155 160

Met Leu

<210> 167
<211> 487
<212> DNA
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR183; Accession DDBJ/EMBL/GenBank = AF179727

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 167
t gtg gcc atc tgt ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1 5 10 15

ctc tgt ctc tcc gtg gtg acg ctg tcc tgg gtg ctg acc acc ttc cat 97
Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
35 40 45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg 193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga 241
Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
65 70 75 80

ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289
 Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95
 aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc 337
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110
 aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc 385
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125
 tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct 433
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
 130 135 140
 act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160
 atg ctg 487
 Met Leu

<210> 168
 <211> 162
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR183; Accession DDBJ/EMBL/GenBank = AF179727

<400> 168
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ser Val Val Thr Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe

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115              120              125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
130              135              140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
145              150              155              160

Met Leu

<210> 169
<211> 487
<212> DNA
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 169
t  gtg gcc atc tgt ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
    1              5              10              15

ctc tgt ctc tcc gtg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
      20              25              30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
      35              40              45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct cta ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
      50              55              60

gcc tgc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga      241
Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
      65              70              75              80

ggg ctc att gtt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
      85              90              95

aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
      100              105              110

aag gcc ttg tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
      115              120              125

tat ggg acc gtt att ggt ctc tac tta tgc cca tca gct aat agt tct      433
Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
      130              135              140

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act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

atg ctg 487
 Met Leu

<210> 170
 <211> 162
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR203; Accession DDBJ/EMBL/GenBank = AF179728

<400> 170
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

Leu Cys Leu Ser Val Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

Gly Leu Ile Val Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser
 130 135 140

Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 171

<211> 485
 <212> DNA
 <213> Pan troglodytes

 <220>
 <221> misc_feature
 <222> (1)..(485)
 <223> Taxon = 9598; gene = PTR204; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179729

<400> 171
 tgtagccata tgtaatccct tgctttatcc agtgatgatg tccaacaaac tcagcgctca 60
 gttgctaagc atttcatatg taattgggtt cctgcaccc ctggttcatg tgagtttact 120
 attgcgacta actttctgca ggtttaacat aatacattat ttctactgtg aaattttaca 180
 actgttcaaa atttcatgca atggtccatc tattaacgca ctaatgatat ttatttttgg 240
 tgcttttata caaataccca ctttaatgac gatcataatc tcttatactc gtgtgctctt 300
 tgatattctg aaaaaaaagt ctgaaaaggg cagaagcaaa gccttctcca catgcagcgc 360
 ccatctgctt tctgtctcat tgtactacgg aactctgac ttcatgtatg tgcgtcctgc 420
 atctggctta gctgaagacc cagacaaagt gtattctctt ttacacgatt ataattcccc 480
 tgcta 485

<210> 172
 <211> 487
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR205; Accession DDBJ/EMBL/GenBank = AF179730

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 172
 t gtg gcc att tgc cgc ccc ctc tgc tac tcc aca gtc acg agg ccc caa 49
 Val Ala Ile Cys Arg Pro Leu Cys Tyr Ser Thr Val Thr Arg Pro Gln
 1 5 10 15

 gtc tgt gcc cta atg ctt gca ttg tgc tgg gtc ctc acc aat atc att 97
 Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
 20 25 30

 gcc ctg act cac acg ttc ctc atg gct cgg ttg tcc ttc tgt gtg act 145
 Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45

 ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag ctg 193
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60

 tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga 241
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80

ggc acc gta ctc atc gtc ccc ttt tta tgc att gtc acc tcc tac atc 289
 Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
 85 90 95
 cac att gtg cca gct atc ctg agg gtc cga acc cgt ggt ggg gtg ggc 337
 His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly
 100 105 110
 aag gcc ttt tcc acc tgc agt tcc cac ctc tgc gtt gtt tgt gtg ttc 385
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe
 115 120 125
 tat ggg acg ctc ttc agt gcc tac ctg tgt cct ccc tcc att gcc tct 433
 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
 130 135 140
 gaa gag aag gac att gca gca gct gca atg tac acc ata gtg act ccc 481
 Glu Glu Lys Asp Ile Ala Ala Ala Met Tyr Thr Ile Val Thr Pro
 145 150 155 160
 atg ttg 487
 Met Leu

<210> 173
 <211> 162
 <212> PRT
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR205; Accession DDBJ/EMBL/GenBank = AF179730

<400> 173
 Val Ala Ile Cys Arg Pro Leu Cys Tyr Ser Thr Val Thr Arg Pro Gln
 1 5 10 15
 Val Cys Ala Leu Met Leu Ala Leu Cys Trp Val Leu Thr Asn Ile Ile
 20 25 30
 Ala Leu Thr His Thr Phe Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80
 Gly Thr Val Leu Ile Val Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
 85 90 95
 His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Arg Gly Gly Val Gly
 100 105 110
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Val Val Cys Val Phe
 115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
 130 135 140

Glu Glu Lys Asp Ile Ala Ala Ala Met Tyr Thr Ile Val Thr Pro
 145 150 155 160

Met Leu

<210> 174
 <211> 487
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR206; Accession DDBJ/EMBL/GenBank = AF179731

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 174
 c gtg gcc atc tgt cac cct tta cat tac tcc acc att atg gcc ctg cgc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
 1 5 10 15
 ctc tgt gcc tct ctg gta gct gca cct tgg gtc att gcc att ttg aac 97
 Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn
 20 25 30
 cct ctc ttg cac act ctt atg atg gcc cat ctg cac ttc tgc tct gat 145
 Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp
 35 40 45
 aat gtt atc cac cat ttc ttc tgt gat atc aac tct ctc ctc cct ctg 193
 Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu
 50 55 60
 tcc tgt tcc aac acc agt ctt aat cag ttg agt gtt ctg gct acg gtg 241
 Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val
 65 70 75 80
 ggg ctg atc ttt gtg gta cct tca gtg tgt atc ctg gta tcc tat atc 289
 Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile
 85 90 95
 ctc att gtt tct gct gtg atg aaa gtc cct tct gcc caa gga aaa ctc 337
 Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu
 100 105 110
 aag gct ttc tct atc tgt gga tct cac ctt gcc ttg gtc att ctt ttc 385
 Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe
 115 120 125
 tat gga gca atc aca ggg gtc tat atg agc ccc tta tcc aat cac tct 433
 Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser
 130 135 140

act gaa aaa gac tca gcc gca tca gtc att ttt atg gtt gta gca cct 481
 Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro
 145 150 155 160

gtg ttg 487
 Val Leu

<210> 175
 <211> 162
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR206; Accession DDBJ/EMBL/GenBank = AF179731

<400> 175
 Val Ala Ile Cys His Pro Leu His Tyr Ser Thr Ile Met Ala Leu Arg
 1 5 10 15

Leu Cys Ala Ser Leu Val Ala Ala Pro Trp Val Ile Ala Ile Leu Asn
 20 25 30

Pro Leu Leu His Thr Leu Met Met Ala His Leu His Phe Cys Ser Asp
 35 40 45

Asn Val Ile His His Phe Phe Cys Asp Ile Asn Ser Leu Leu Pro Leu
 50 55 60

Ser Cys Ser Asn Thr Ser Leu Asn Gln Leu Ser Val Leu Ala Thr Val
 65 70 75 80

Gly Leu Ile Phe Val Val Pro Ser Val Cys Ile Leu Val Ser Tyr Ile
 85 90 95

Leu Ile Val Ser Ala Val Met Lys Val Pro Ser Ala Gln Gly Lys Leu
 100 105 110

Lys Ala Phe Ser Ile Cys Gly Ser His Leu Ala Leu Val Ile Leu Phe
 115 120 125

Tyr Gly Ala Ile Thr Gly Val Tyr Met Ser Pro Leu Ser Asn His Ser
 130 135 140

Thr Glu Lys Asp Ser Ala Ala Ser Val Ile Phe Met Val Val Ala Pro
 145 150 155 160

Val Leu

<210> 176
 <211> 487

<212> DNA
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 176
 t gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tac cag agg 49
 Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
 1 5 10 15
 ctt tgc tcc ttg ttg gtg gct aca tca tac tgt tgg ggg aga gtc tgt 97
 Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
 20 25 30
 tcc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat 145
 Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 35 40 45
 aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg 193
 Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
 50 55 60
 tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc 241
 Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
 65 70 75 80
 aca ttc aat gaa ata agc agc ctg gtg atc act ctc act tcc tat gct 289
 Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
 85 90 95
 ttc att ttt atc act gtc atg aag acg gct tcc att ggg ggg cgc aag 337
 Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
 100 105 110
 aaa gcg ttc ttc acg tgt gcc tcc cac ttg acg gcc att acc att ttc 385
 Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
 115 120 125
 cat ggg act att ctt ttc ctc tac tgt gtt cct aac tcc aaa agt tcg 433
 His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
 130 135 140
 tgg ctc atg gtc aag gtg gcc tct gtc ttt tac aca gtg gtc att ccc 481
 Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
 145 150 155 160
 atg ctg 487
 Met Leu

<210> 177
 <211> 162
 <212> PRT
 <213> Pan troglodytes

<220>
 <221> misc_feature

<222> (1)..(487)
 <223> Taxon = 9598; gene = PTR207; Accession DDBJ/EMBL/GenBank = AF179732

<400> 177
 Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Tyr Gln Arg
 1 5 10 15

Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Cys Trp Gly Arg Val Cys
 20 25 30

Ser Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
 35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
 50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
 65 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Val Ile Thr Leu Thr Ser Tyr Ala
 85 90 95

Phe Ile Phe Ile Thr Val Met Lys Thr Ala Ser Ile Gly Gly Arg Lys
 100 105 110

Lys Ala Phe Phe Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
 115 120 125

His Gly Thr Ile Leu Phe Leu Tyr Cys Val Pro Asn Ser Lys Ser Ser
 130 135 140

Trp Leu Met Val Lys Val Ala Ser Val Phe Tyr Thr Val Val Ile Pro
 145 150 155 160

Met Leu

<210> 178
 <211> 481
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(481)
 <223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733

<220>
 <221> CDS
 <222> (2)..(481)
 <223> Product = olfactory receptor

<400> 178
 c ctg gca ata tgt cag ccc ctg cgc tac cca gtg ctc atg aat ggg agg 49
 Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg

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1           5           10          15
tta tgc aca gtc ctt gtg gct gga gct tgt gtc gcc ggc tcc atg cat    97
Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His
                20                25                30

ggg tct atc cag gcc acc ctg acc ttc cgc ctg ccc tac tgt ggg ccc    145
Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
                35                40                45

aat cag gtg gat tac ttt atc tgt gac atc ccc gca gta ttg aga ctg    193
Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
                50                55                60

gcc tgt gct gac aca act gtc aat gag ctt gtg acc ttt gtg gac gtc    241
Ala Cys Ala Asp Thr Thr Val Asn Glu Leu Val Thr Phe Val Asp Val
        65                70                75                80

ggg gtg gtg gcc gcc agt tgc ttc atg tta att ctg ctc tcg tat gcc    289
Gly Val Val Ala Ala Ser Cys Phe Met Leu Ile Leu Leu Ser Tyr Ala
                85                90                95

aac ata gta aat gcc atc ctg aag ata cgc acc act gat ggg agg cac    337
Asn Ile Val Asn Ala Ile Leu Lys Ile Arg Thr Thr Asp Gly Arg His
                100                105                110

cgg gcc ttc tcc acc tgt ggc tcc cac cta atc gtg gtc aca gtc tac    385
Arg Ala Phe Ser Thr Cys Gly Ser His Leu Ile Val Val Thr Val Tyr
                115                120                125

tat gtc ccc tgt att ttc atc tac ctt agg gct ggc tcc aaa ggc ccc    433
Tyr Val Pro Cys Ile Phe Ile Tyr Leu Arg Ala Gly Ser Lys Gly Pro
                130                135                140

ctg gat ggg gcg gcg gct gtg ttt tac act gtt gtc act cca tta ctg    481
Leu Asp Gly Ala Ala Val Phe Tyr Thr Val Val Thr Pro Leu Leu
        145                150                155                160

<210> 179
<211> 160
<212> PRT
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(481)
<223> Taxon = 9598; gene = PTR208; Accession DDBJ/EMBL/GenBank = AF179733

<400> 179
Leu Ala Ile Cys Gln Pro Leu Arg Tyr Pro Val Leu Met Asn Gly Arg
1           5           10          15

Leu Cys Thr Val Leu Val Ala Gly Ala Cys Val Ala Gly Ser Met His
                20                25                30

Gly Ser Ile Gln Ala Thr Leu Thr Phe Arg Leu Pro Tyr Cys Gly Pro
                35                40                45

Asn Gln Val Asp Tyr Phe Ile Cys Asp Ile Pro Ala Val Leu Arg Leu
        50                55                60

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100      105      110
aaa gcc ttt tct acc tgt gga tct cat ctg ttt gtg gtt tct tta ttc      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe
115      120      125

tat ggg aca ggc ctt ggt gtg tat ctt agt tcc aat gca tcg tcc tct      433
Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
130      135      140

tcc tgg tgg ggc atg gtg gcc tcg gtc atg tac act gtg gtc acc ccc      481
Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
145      150      155      160

atg ctg      487
Met Leu

<210> 181
<211> 162
<212> PRT
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR209; Accession DDBJ/EMBL/GenBank = AF179734

<400> 181
Val Ala Ile Cys His Pro Leu Tyr Tyr Arg Val Ile Val Asn Pro Arg
1      5      10      15

Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
20      25      30

Ser Leu Ile Gln Ser Leu Leu Met Leu Gln Val Ser Phe Cys Thr Ser
35      40      45

Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
50      55      60

Thr Cys Ser Asp Thr His Val Asn Tyr Ile Leu Leu Tyr Val Val Thr
65      70      75      80

Gly Leu Leu Asp Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
85      90      95

Gln Ile Val Ser Tyr Ile Leu Arg Ile Ser Ser Thr Asp Gly Lys His
100      105      110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Phe Val Val Ser Leu Phe
115      120      125

Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
130      135      140

```

Ser Trp Trp Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 182
 <211> 487
 <212> DNA
 <213> Pan troglodytes
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 182
 t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa 49
 Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
 1 5 10 15
 ctc agc gct cag ttg cta agc att tca tat gta att ggt ttc ctg cat 97
 Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
 20 25 30
 cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt 145
 Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
 35 40 45
 aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att 193
 Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50 55 60
 tca tgc aat ggt cca tct att aac gca cta atg ata ttt att ttt ggt 241
 Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
 65 70 75 80
 gct ttt ata caa ata ccc act tta atg acg atc ata atc tct tat tct 289
 Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
 85 90 95
 cgt gtg ctc ttt gat att ctg aaa aaa aag tct gaa aag ggc aga agc 337
 Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
 100 105 110
 aaa gcc ttc tcc aca tgc agc gcc cat ctg ctt tct gtc tca ttg tac 385
 Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
 115 120 125
 tac gga act ctg atc ttc atg tat gtg cgt cct gca tct ggc tta gct 433
 Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
 130 135 140
 gaa gac cca gac aaa gtg tat tct ctg ttt tac acg att ata att ccc 481
 Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
 145 150 155 160
 ctg cta 487
 Leu Leu

<210> 183
 <211> 162
 <212> PRT
 <213> Pan troglodytes

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9598; gene = PTR210; Accession DDBJ/EMBL/GenBank = AF179735

<400> 183
 Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
 1 5 10 15

Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
 20 25 30

Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
 35 40 45

Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
 50 55 60

Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Met Ile Phe Ile Phe Gly
 65 70 75 80

Ala Phe Ile Gln Ile Pro Thr Leu Met Thr Ile Ile Ile Ser Tyr Ser
 85 90 95

Arg Val Leu Phe Asp Ile Leu Lys Lys Lys Ser Glu Lys Gly Arg Ser
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ala His Leu Leu Ser Val Ser Leu Tyr
 115 120 125

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
 130 135 140

Glu Asp Pro Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
 145 150 155 160

Leu Leu

<210> 184
 <211> 487
 <212> DNA
 <213> Pan troglodytes

<220>
 <221> misc_feature
 <222> (1)..(487)

<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 184

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t gtg gcc att tgc cac cca ctg agg tac aca gtc ctc atg aac atc cat      49
  Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
    1             5             10             15

ttc tgc ggc ttg ctg att ctt ctc tcc agg ttc atg agc act atg gat      97
Phe Cys Gly Leu Leu Ile Leu Leu Ser Arg Phe Met Ser Thr Met Asp
    20             25             30

gcc ctg gtt cag agt ctg atg ata ttt cag ctg tcc ttc tgc aaa aac      145
Ala Leu Val Gln Ser Leu Met Ile Phe Gln Leu Ser Phe Cys Lys Asn
    35             40             45

gtt gaa atc cct ttg ttc ttc tgt gaa gtc gtt cag gtc atc aag ctc      193
Val Glu Ile Pro Leu Phe Phe Cys Glu Val Val Gln Val Ile Lys Leu
    50             55             60

gcc tgt tct gac acc ctc atc aac aac atc ctc ata tat ttt gca agt      241
Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ser
    65             70             75             80

agc ata ttt ggt gca att cct ctc tct gga ata att ttc tct tat tct      289
Ser Ile Phe Gly Ala Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ser
    85             90             95

caa ata gtc acc tct gtt ctg aga atg cca tca gca aga gga aag tat      337
Gln Ile Val Thr Ser Val Leu Arg Met Pro Ser Ala Arg Gly Lys Tyr
   100             105             110

aaa gcg ttt tcc acc tgt ggc tgt cac ctc tct gtt ttt tcc ttg ttc      385
Lys Ala Phe Ser Thr Cys Gly Cys His Leu Ser Val Phe Ser Leu Phe
   115             120             125

tat ggg aca gct ttt ggg gtg tcc att agt tct gct gtt gct gag tct      433
Tyr Gly Thr Ala Phe Gly Val Ser Ile Ser Ser Ala Val Ala Glu Ser
   130             135             140

tcc cga att act gct gtg ggt tca gtg atg tac act gtg gtc cca caa      481
Ser Arg Ile Thr Ala Val Gly Ser Val Met Tyr Thr Val Val Pro Gln
   145             150             155             160

atg atg
Met Met      487
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<210> 185

<211> 162

<212> PRT

<213> Pan troglodytes

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9598; gene = PTR211; Accession DDBJ/EMBL/GenBank = AF179736

<400> 185

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Val Ala Ile Cys His Pro Leu Arg Tyr Thr Val Leu Met Asn Ile His
1             5             10             15
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tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35                        40                        45

aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50                        55                        60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65                        70                        75

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85                        90                        95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100                       105                       110

aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115                       120                       125

tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130                       135                       140

att gac aag gat gtc att gtg gct ctc atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
      145                       150                       155                       160

atg ttg
Met Leu
      487

<210> 187
<211> 162
<212> PRT
<213> Pan troglodytes

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9598; gene = PTR212; Accession DDBJ/EMBL/GenBank = AF179737

<400> 187
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1      5      10      15

Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
      20      25      30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35      40      45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50      55      60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65      70      75      80

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Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 188
<211> 484
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA121; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179738

<400> 188
tgtggctatc tgcctgccgc ttaggtatcc agagctcatg agtgggcaga cctgcatgca 60
gatggcagca ctgagctggg ggacaggctt tgccaactca ctgctacagt ccatccttgt 120
ctggcgccctc cctttctgtg gccacaacgt catcaaccac tttttctgtg agatcttggc 180
agtgctaaaa ctggcctgtg gggacatctc cctcaatgcg ctggcattaa tgggtggccac 240
agctgtcctg aactggccc ccctcttgc tcatctgctg tcttaccttt tcatcttgtc 300
tgccatcctt agggtagcct ctgctgcagg ccggcgcaaa gccttctcca cctgctcagc 360
ccacctcaca gtggtggtgg ttttttaagg gacaatttcc ttcattgtact tcaaacccaa 420
ggccaaggac cccaacgtgg ataagattgt tgcattgttg tatgggggtg tgacaccctc 480
gctg 484

<210> 189
<211> 487
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

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<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 189
t  gtg gcg gtg tgt aac cct ctt ctc tac aca gtt gca atg tcc cag agg      49
  Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
    1              5              10              15

ctt tgc tcc ttg ttg gtg gct aca tca tac tct tgg ggg ata gtc tgt      97
Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
          20              25              30

ttc ctg aca ctt acc tac ttt cta ctg gaa tta tcc ttc aga gga aat      145
Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
          35              40              45

aat atc att aat aac ttt gtc tgt gag cat gct gcc att gtt gct gtg      193
Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
          50              55              60

tct tgc tct gac ccc tat gtg agc cag gag atc act tta gtt tct gcc      241
Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
        65              70              75              80

aca ttc aat gaa ata agc agt ctg atg atg att ttc act tcc tat gct      289
Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
          85              90              95

ttc att ttt atc act gtc atg aag atg cct tcc act ggg ggg cgc aag      337
Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
          100              105              110

aaa gcg ttc tcc acg tgt gcc tcc cac ctg acc gcc att acc att ttc      385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
          115              120              125

cat ggg act atc ctt ttc ccc tac tgt gtt cct aac tcc aaa agt tca      433
His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
          130              135              140

tgg ctc atg gtc aag gtg acc tct gtc ttt tac aca gtg ttc att ccc      481
Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
          145              150              155              160

atg gtg      487
Met Val

<210> 190
<211> 162
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA122; Accession DDBJ/EMBL/GenBank = AF179739

<400> 190
Val Ala Val Cys Asn Pro Leu Leu Tyr Thr Val Ala Met Ser Gln Arg
  1              5              10              15

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Leu Cys Ser Leu Leu Val Ala Thr Ser Tyr Ser Trp Gly Ile Val Cys
20 25 30

Phe Leu Thr Leu Thr Tyr Phe Leu Leu Glu Leu Ser Phe Arg Gly Asn
35 40 45

Asn Ile Ile Asn Asn Phe Val Cys Glu His Ala Ala Ile Val Ala Val
50 55 60

Ser Cys Ser Asp Pro Tyr Val Ser Gln Glu Ile Thr Leu Val Ser Ala
65 70 75 80

Thr Phe Asn Glu Ile Ser Ser Leu Met Met Ile Phe Thr Ser Tyr Ala
85 90 95

Phe Ile Phe Ile Thr Val Met Lys Met Pro Ser Thr Gly Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Ala Ile Thr Ile Phe
115 120 125

His Gly Thr Ile Leu Phe Pro Tyr Cys Val Pro Asn Ser Lys Ser Ser
130 135 140

Trp Leu Met Val Lys Val Thr Ser Val Phe Tyr Thr Val Phe Ile Pro
145 150 155 160

Met Val

<210> 191
<211> 486
<212> DNA
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740

<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor

<400> 191
t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145
Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp

```

          35              40              45
cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg      193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
   50              55              60

tcc tgc tca gat acc tcc ctc aat cag ttg gca atc ttt aca gca gga      241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
   65              70              75              80

ttg aca gcc att atg ctt cca ttc ttg tgc atc ctg gtt tct tat ggt      289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
              85              90              95

cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc      337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
              100              105              110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
              115              120              125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
              130              135              140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc      481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
              145              150              155              160

atg tt      486
Met

<210> 192
<211> 161
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9580; gene = HLA123; Accession DDBJ/EMBL/GenBank = AF179740

<400> 192
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1              5              10              15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
              20              25              30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
              35              40              45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50              55              60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65              70              75              80

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

 His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
 100 105 110

 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
 115 120 125

 Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

 Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met

<210> 193
 <211> 487
 <212> DNA
 <213> Hylobates lar

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA124; Accession DDBJ/EMBL/GenBank = AF179741

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 193
 t gtg gcc atc tgt agt ccc ttg cac tac cca gtc atc atg aac caa agg 49
 Val Ala Ile Cys Ser Pro Leu His Tyr Pro Val Ile Met Asn Gln Arg
 1 5 10 15

 act cgt gcc aaa ctg gct gct gcc tcc tgg ttc cca ggc ttt cct gta 97
 Thr Arg Ala Lys Leu Ala Ala Ala Ser Trp Phe Pro Gly Phe Pro Val
 20 25 30

 gct act gtg cag acc aca tgg ctc ttc agt ttt cca ttc tgt ggc acc 145
 Ala Thr Val Gln Thr Thr Trp Leu Phe Ser Phe Pro Phe Cys Gly Thr
 35 40 45

 aac aag gta aac cac ttc ttc tgt gac agc ccg cct gtg ctg agg ctg 193
 Asn Lys Val Asn His Phe Phe Cys Asp Ser Pro Pro Val Leu Arg Leu
 50 55 60

 gtc tgt gca gac aca gca ctg ttt gag atc tac gcc atc gtc gga acc 241
 Val Cys Ala Asp Thr Ala Leu Phe Glu Ile Tyr Ala Ile Val Gly Thr
 65 70 75 80

 att ctg gtg gtc atg atc cct tgc ttg ctg atc ttg tgt tcc tat act 289
 Ile Leu Val Val Met Ile Pro Cys Leu Leu Ile Leu Cys Ser Tyr Thr
 85 90 95

 cac att gct gct gcc atc ctc aag atc cca tcg gct aaa ggg aag aat 337
 His Ile Ala Ala Ala Ile Leu Lys Ile Pro Ser Ala Lys Gly Lys Asn

Pro Glu Gly Lys Lys Leu Leu Ser Leu Ser Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 195
 <211> 487
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 195
 t gtg gcc atc tgc aag cct ctg cat tac ttg aat atc atg aat cga aga 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
 1 5 10 15
 gtc tgc ata ctg ctt gtt ttt act tct tgg ctg att tca ttc tta atc 97
 Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
 20 25 30
 ata ttc cct gca ctc atg ttg ctc tta aag ctt gat tac tgt agg tct 145
 Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
 35 40 45
 aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg caa ctt 193
 Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60
 gct tgt tca gac aca aaa ttc tta gag gtg atg gca ttt tct tgt gct 241
 Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
 65 70 75 80
 gtg ttt act cta atg ttc act ttg gca tta ata tct ctg tcc tac ata 289
 Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
 85 90 95
 tac att atc aga aca att ttg aga att cct tct act agt cag agg aca 337
 Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
 100 105 110
 aag gcc ttt tcc aca tgt tct tcc cac atg gtt gtt att tcc atc tct 385
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
 115 120 125
 tat ggc agc tgc att ttt atg tac att aaa ccc tca gca aaa gat aga 433
 Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
 130 135 140
 gtg tcc ttg agc aag gga gtg gca ata cta aac acc tca gta gcc ccc 481
 Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
 145 150 155 160
 atg atg 487
 Met Met

<210> 196
 <211> 162
 <212> PRT
 <213> Hylobates lar

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA125; Accession DDBJ/EMBL/GenBank = AF179742

<400> 196
 Val Ala Ile Cys Lys Pro Leu His Tyr Leu Asn Ile Met Asn Arg Arg
 1 5 10 15

Val Cys Ile Leu Leu Val Phe Thr Ser Trp Leu Ile Ser Phe Leu Ile
 20 25 30

Ile Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Arg Ser
 35 40 45

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
 50 55 60

Ala Cys Ser Asp Thr Lys Phe Leu Glu Val Met Ala Phe Ser Cys Ala
 65 70 75 80

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Ser Leu Ser Tyr Ile
 85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Val Val Ile Ser Ile Ser
 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
 130 135 140

Val Ser Leu Ser Lys Gly Val Ala Ile Leu Asn Thr Ser Val Ala Pro
 145 150 155 160

Met Met

<210> 197
 <211> 484
 <212> DNA
 <213> Hylobates lar

<220>
 <221> misc_feature
 <222> (1)..(484)

gct	ctt	ttg	cat	acc	ctc	ctc	ctg	gcc	cag	ctt	tcc	ttt	tgt	gct	gac	145
Ala	Leu	Leu	His	Thr	Leu	Leu	Leu	Ala	Gln	Leu	Ser	Phe	Cys	Ala	Asp	
	35						40					45				
cac	atc	atc	cct	cac	ttc	ttc	tgt	gac	ctt	ggc	ctg	ctc	aag	ttg		193
His	Ile	Ile	Pro	His	Phe	Phe	Cys	Asp	Leu	Gly	Ala	Leu	Leu	Lys	Leu	
	50					55					60					
tcc	tgc	tca	gat	acc	tcc	ctc	aat	cag	ttg	gca	atc	ttt	aca	gca	gga	241
Ser	Cys	Ser	Asp	Thr	Ser	Leu	Asn	Gln	Leu	Ala	Ile	Phe	Thr	Ala	Gly	
65					70					75					80	
ttg	aca	gcc	att	atg	ctt	cca	ttc	ttg	tgc	atc	ctg	gtt	tct	tat	ggc	289
Leu	Thr	Ala	Ile	Met	Leu	Pro	Phe	Leu	Cys	Ile	Leu	Val	Ser	Tyr	Gly	
				85					90					95		
cac	att	ggg	gtc	acc	atc	ctc	cag	att	ccc	tct	acc	aag	ggc	ata	tgc	337
His	Ile	Gly	Val	Thr	Ile	Leu	Gln	Ile	Pro	Ser	Thr	Lys	Gly	Ile	Cys	
			100					105					110			
aaa	gcc	ttg	tcc	att	tgt	gga	tcc	cac	ctc	tca	gtg	gtg	act	atc	tat	385
Lys	Ala	Leu	Ser	Ile	Cys	Gly	Ser	His	Leu	Ser	Val	Val	Thr	Ile	Tyr	
		115					120					125				
tat	ggg	aca	att	att	ggc	ctc	tat	ttt	ctt	ccc	cca	tcc	agc	aac	acc	433
Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr	Phe	Leu	Pro	Pro	Ser	Ser	Asn	Thr	
	130					135					140					
aat	gac	aag	aac	ata	att	gct	tca	gtg	ata	tac	aca	gta	gtc	act	ccc	481
Asn	Asp	Lys	Asn	Ile	Ile	Ala	Ser	Val	Ile	Tyr	Thr	Val	Val	Thr	Pro	
145					150					155					160	
atg	ttg															487
Met	Leu															
<210>	200															
<211>	162															
<212>	PRT															
<213>	Hylobates lar															
<220>																
<221>	misc_feature															
<222>	(1)..(487)															
<223>	Taxon = 9580; gene = HLA127; Accession DDBJ/EMBL/GenBank = AF179744															
<400>	200															
Val	Ala	Ile	Cys	His	Pro	Leu	His	Tyr	Ala	Thr	Ile	Met	Ser	Gln	Ser	
1				5					10					15		
Gln	Cys	Val	Met	Leu	Val	Ala	Gly	Ser	Trp	Val	Ile	Ala	Cys	Ala	Cys	
			20					25					30			
Ala	Leu	Leu	His	Thr	Leu	Le										

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337
 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
 100 105 110

 aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat 385
 Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
 115 120 125

 ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att 433
 Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
 130 135 140

 gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg 481
 Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
 145 150 155 160

 ttg 484
 Leu

<210> 202
 <211> 161
 <212> PRT
 <213> Hylobates lar

 <220>
 <221> misc_feature
 <222> (1)..(484)
 <223> Taxon = 9580; gene = HLA128; Accession DDBJ/EMBL/GenBank AF179745

<400> 202
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15

 Leu Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
 20 25 30

 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45

 Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
 100 105 110

 Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
 115 120 125

 Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
 130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
 145 150 155 160

Leu

<210> 203
 <211> 484
 <212> DNA
 <213> Hylobates lar
 <220>
 <221> misc_feature
 <222> (1)..(484)
 <223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746

<220>
 <221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor

<400> 203
 t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15
 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30
 gct ctt ttg cat acc ctc ctc ctg gcc cag ctt tcc ttt tgt gct gac 145
 Ala Leu Leu His Thr Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
 35 40 45
 cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg 193
 His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60
 tcc tgc tca gat acc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
 Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80
 gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95
 tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337
 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
 100 105 110
 aaa gcg tcc acg tgt ggc tcc cat ctt tct gtg gtg tct ctc tat tat 385
 Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
 115 120 125
 ggg tca ata ttt ggc cag tac ctt ttc ccg acc gca agc agt tcc att 433
 Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
 130 135 140
 gac aag gat gtc att gtg gct gtc atg tac aca gtg atc aca ccc atg 481
 Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
 145 150 155 160

ttg
Leu

484

<210> 204
<211> 161
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9580; gene = HLA129; Accession DDBJ/EMBL/GenBank = AF179746

<400> 204
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
100 105 110

Lys Ala Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr Tyr
115 120 125

Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Ala Ser Ser Ser Ile
130 135 140

Asp Lys Asp Val Ile Val Ala Val Met Tyr Thr Val Ile Thr Pro Met
145 150 155 160

Leu

<210> 205
<211> 486
<212> DNA
<213> Hylobates lar

<220>

<221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9580; gene = HLA130; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179747

<400> 205
 tgtggccatc tgtcaccctc tacattatgc accatcatga gtcagagcca gtgtgtcatg 60
 ctggtggctg ggtcctgggt catcgcttgt gcgtgtgctc ttttgcatac cctcctcctg 120
 gccagccttt ccttttgtgc tgaccacatc atccctcact tcttctgtga ccttggtgcc 180
 ctgctcaagt tgtcctgctc agatacctcc ctcaatcagt tggcaatctt tacagcagga 240
 ttgacagcca ttatgcttcc attcctgtgc atcctggttt cttatggtca cattggggtc 300
 accatcctcc agattccctc taccaagggc atatgcaaag ccttgtccat ttgtggatcc 360
 cacctctcag tgggtgactat ctattatggg acaattattg gtctctatct tcttccccca 420
 tccagcaaca ccaatgacaa gaacataatt gcttcagtga tatacacagt agtcactccc 480
 atgttg 486

<210> 206
 <211> 487
 <212> DNA
 <213> Hylobates lar

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA131; Accession DDBJ/EMBL/GenBank = AF179748

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 206
 t gtg gcc atc tgt cgc ccc ctg tac tac cct gtc atc atg aaa cct cac 49
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
 1 5 10 15
 ctc tgt ggc ctg ctg gtt ctt gtg tcc tgg ttc ctc agc ttg tca tac 97
 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
 20 25 30
 tcc ctg atc cag agt ctg ttg atg ctg cgg gtg tcc ttc tgc acc agt 145
 Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
 35 40 45
 tgg gtc att cag cac ttt tac tgt gag ctt gct cag gtc ctc acg ctt 193
 Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
 50 55 60
 gcc tgc tca gac aca cac atc aat tac atc ctg ctc tac atg gtg acc 241
 Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
 65 70 75 80
 ggc ctt ttg ggc ttt gtg ccc ttc tca ggg atc ctt ttc tcc tac acc 289
 Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
 85 90 95
 caa atc gtc tcc tcc atc ctg aga atc tca tcc cca gat ggg aaa cac 337

Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His
 100 105 110
 aaa gcc ttt tct acc tgt gga tct cat ctg tct gtg gtt tct tta ttc 385
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125
 tat ggg aca ggt ctt ggc gtg tat ctt agt tcc aat gca tcg tcc tct 433
 Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
 130 135 140
 tcc tgg cgg ggc atg gtg gct tcc gta atg tac act gtg gta acc ccc 481
 Ser Trp Arg Gly Met Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160
 aat gtg 487
 Asn Val

 <210> 207
 <211> 162
 <212> PRT
 <213> Hylobates lar

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9580; gene = HLA131; Accession DDBJ/EMBL/GenBank = AF179748

 <400> 207
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Pro Val Ile Met Lys Pro His
 1 5 10 15
 Leu Cys Gly Leu Leu Val Leu Val Ser Trp Phe Leu Ser Leu Ser Tyr
 20 25 30
 Ser Leu Ile Gln Ser Leu Leu Met Leu Arg Val Ser Phe Cys Thr Ser
 35 40 45
 Trp Val Ile Gln His Phe Tyr Cys Glu Leu Ala Gln Val Leu Thr Leu
 50 55 60
 Ala Cys Ser Asp Thr His Ile Asn Tyr Ile Leu Leu Tyr Met Val Thr
 65 70 75 80
 Gly Leu Leu Gly Phe Val Pro Phe Ser Gly Ile Leu Phe Ser Tyr Thr
 85 90 95
 Gln Ile Val Ser Ser Ile Leu Arg Ile Ser Ser Pro Asp Gly Lys His
 100 105 110
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125
 Tyr Gly Thr Gly Leu Gly Val Tyr Leu Ser Ser Asn Ala Ser Ser Ser
 130 135 140

Met Leu

<210> 209
<211> 162
<212> PRT
<213> Hylobates lar

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9580; gene = HLA132; Accession DDBJ/EMBL/GenBank = AF179749

<400> 209
Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Gln Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Thr Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Ile Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 210
<211> 487
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature

<222> (1)..(487)
 <223> Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 210
 t gta gcc att tgt cat cct ctt cat tat acc ttc att atg gac caa aac 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn
 1 5 10 15
 acc tgc att caa ctg gca gtt att tct tgg tcc agt agc ttc ctg tgt 97
 Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
 20 25 30
 tcc atg gtt atc aat gtt ctc acg ttg agt ttg ccc tac tgt ggg cct 145
 Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
 35 40 45
 aat atc ctg aat cac ttt ttc tgt gag gta cct act gtc ctg agg ttg 193
 Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
 50 55 60
 tct tgc acc gac acc tca ttc acg gag ctg gtt gtt ttt atc ttc agt 241
 Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
 65 70 75 80
 atc atc att gtc ttc atc cct ttc ctc ctc att gtt gtt tcc tat gtc 289
 Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
 85 90 95
 cgg atc ctt caa tct gtt ctc agg atg cgg tca gcc tcc ggg cgg tat 337
 Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
 100 105 110
 aag gca tta tcc acc tgt acc tcc cat ttg aca gtg gta acc tta ttt 385
 Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
 115 120 125
 tat ggg act gcc atc ctc atg tac atg aga cca cag tgc agg tct tcc 433
 Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
 130 135 140
 tgg gct ggc ggc aag atc att gcg gtt ttc tac acg gtg gtc aca ccc 481
 Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
 145 150 155 160
 atg ctt 487
 Met Leu

<210> 211
 <211> 162
 <212> PRT
 <213> Gorilla gorilla
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9593; gene = GGO100; Accession DDBJ/EMBL/GenBank = AF179750
 <400> 211
 Val Ala Ile Cys His Pro Leu His Tyr Thr Phe Ile Met Asp Gln Asn


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1           5           10           15

Thr Cys Ile Gln Leu Ala Val Ile Ser Trp Ser Ser Ser Phe Leu Cys
20           25           30

Ser Met Val Ile Asn Val Leu Thr Leu Ser Leu Pro Tyr Cys Gly Pro
35           40           45

Asn Ile Leu Asn His Phe Phe Cys Glu Val Pro Thr Val Leu Arg Leu
50           55           60

Ser Cys Thr Asp Thr Ser Phe Thr Glu Leu Val Val Phe Ile Phe Ser
65           70           75           80

Ile Ile Ile Val Phe Ile Pro Phe Leu Leu Ile Val Val Ser Tyr Val
85           90           95

Arg Ile Leu Gln Ser Val Leu Arg Met Arg Ser Ala Ser Gly Arg Tyr
100          105          110

Lys Ala Leu Ser Thr Cys Thr Ser His Leu Thr Val Val Thr Leu Phe
115          120          125

Tyr Gly Thr Ala Ile Leu Met Tyr Met Arg Pro Gln Ser Arg Ser Ser
130          135          140

Trp Ala Gly Gly Lys Ile Ile Ala Val Phe Tyr Thr Val Val Thr Pro
145          150          155          160

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Met Leu

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<210> 212
<211> 488
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9593; gene = GGO101; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179751

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<400> 212
tgtggccatt agccacccac ttcactatcc catcctcatg aatcagaggg tctgtctcca      60
gattaccggg agctcctggg cctttgggat aatcgatggc tttgatccag atggtggtag      120
taatgaattt ccctactgtg ggcttgagga aggtgaacca tttcttctgt gagatgctat      180
ccttgttgaa gctggcctgt gtagacacat ccctgtttga gaaggtgata tttgcttgct      240
gtgtcttcat gcttctcttc ccattctcca tcatcgtggc ctctatgct cgcattctag      300
ggactgtgct gcaaatgcac tctgctcagg cctggaaaaa ggccctggcc acctgctcct      360

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ccccctgac agctgtcacc ctcttctatg gggcagccat gttcatctac ctgaggccta      420
ggcgctaccg ggcccccagc catgacaagg tggcctctat cttctacaca gtccttactc      480
ccatgctg                                          488

<210> 213
<211> 487
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9593; gene = GGO102; Accession DDBJ/EMBL/GenBank = AF179752

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 213
t gtt gtc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag      49
  Val Val Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
    1             5             10             15

ttc tgt gtc ttc tta gtg gct gta tct tgg att ctg tct tgt gcc agc      97
Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
          20             25             30

tcc ctc tct cac acc gtt ctc ctg acc cag ctg tct ttc tgt gct gcg      145
Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
          35             40             45

aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
          50             55             60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
          65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggt      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
          85             90             95

tac att ggg gcc acc atc ctg ggg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His
          100            105            110

aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
          115            120            125

tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt ttt      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
          130            135            140

att gac aag gat gtc att gtg gct ctc atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
          145            150            155            160

acg ttg                                          487
Thr Leu

```

<210> 214
 <211> 162
 <212> PRT
 <213> Gorilla gorilla

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9593; gene = GGO102; Accession DDBJ/EMBL/GenBank = AF179752

 <400> 214

Val Val Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15

Phe Cys Val Phe Leu Val Ala Val Ser Trp Ile Leu Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Val Leu Leu Thr Gln Leu Ser Phe Cys Ala Ala
 35 40 45

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Gly Val Pro Ser Thr Lys Gly Ile His
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Phe
 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Thr Leu

<210> 215
 <211> 488
 <212> DNA
 <213> Gorilla gorilla

<220>
 <221> misc_feature

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<222> (1)..(488)
<223> Taxon = 9593; gene = GGO103; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179753

<400> 215
tgcggtgtc tgccaccac tccgatatcc cactctcatg agctggcagc tgtgcctgag      60
gataaccatg ttgtcttggc tcctgggtgc agctgacggg ctcatgcagg ctgttgctac      120
cctgagcttc ccatattgcg gtgcacacga gatcgatcac ttcttctgag agggcccccg      180
gctgggttcat ttggcttgtg ctgacacttc agtcttcgaa aacgccatgt acatctgctg      240
tgtgttaatg ctctgggtcc ccttttccct catcctgtcc tcctatggtc tcatcctcgc      300
tgctgttctg cacatgcgct ctacagaagc ccgcaagaag gcctttgcca cctgctcttc      360
acatttggct gtggtgggac tcttttatgg agctgccatt tttacctata tgagacccaa      420
atcccacagg tccactaacc acgataaggt tgtgtcagcc ttctatagta tgttcacccc      480
tttactaa                                         488

<210> 216
<211> 458
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(458)
<223> Taxon = 9593; gene = GGO104; pseudogene; Accession DDBJ/EMBL/ GenBank
= AF179754

<400> 216
ccaccatcat gagtcacagc cagtgtgtca tgctgggtggc tgggtcctgg gtcacgctt      60
gtgcgtgtgc tcttttgcac accctcctcc tggcccggtt ttcttctgt gctgaccaca      120
tcacccctca cttcttctgt gaccttgggtg cctgtctcaa gttgtcctgc tcagacacct      180
ccctcaatca gttagcaatc tttacagcag gattgacagc cattatgctt ccattcctgt      240
gcatcctggg ttcttatggg cacattgggg tcaccatcct ccagattccc tctaccaagg      300
gcatatgcaa agccttgtcc acttgtggat cccacctctc agtggtgact atctattatg      360
ggacaattat tgggtctctat tttcttcccc catcctgcaa caccaatgac gagaacataa      420
ttgcttcagt gatatacaca gtagtcactc ccatattg                                         458

<210> 217
<211> 477
<212> DNA
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(477)
<223> Taxon = 9593; gene = GGO106; Accession DDBJ/EMBL/GenBank = AF179755

<220>
<221> CDS
<222> (2)..(475)

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<223> Product = olfactory receptor

<400> 217

t gtg gcc atc cgt aag ccc ttg cat tat ttg gtt atc atg aga caa tgg 49
Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
1 5 10 15

gtg tgt gtt gtg ctg ctg gta atg tcc tgg gtt gga gga ttt ctg cac 97
Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
20 25 30

tca gta ttt caa ctt agc att att tat ggg ctc cca ttc tgt ggc ccc 145
Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
35 40 45

aat gtc att gat cac ttt ttc tgt gac atg tat ccc tta ttg aaa ctg 193
Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
50 55 60

gtc tgc act gac acc cat gtt att ggc ctc tta gtg gtg acc aat gga 241
Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
65 70 75 80

gga ctg tct tgc act att gtg ttt ctg ctc tta ctc atc tct tat ggt 289
Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Leu Ile Ser Tyr Gly
85 90 95

gtc atc ttg cac tct cta aag aaa ctt agt cag aaa ggg agg caa aaa 337
Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
100 105 110

gcc ctc tca acc tgc agt tcc cac atc act gtg gtt gtc ttc ttc ttt 385
Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe Phe
115 120 125

gtt cct tgt att ttt atg tat gct aga cct gct agg agc ttc ccc att 433
Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
130 135 140

gac aaa tca gtg agt gtg ttt tat aca gtc ata acc cca atg ct 477
Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
145 150 155

<210> 218

<211> 158

<212> PRT

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(477)

<223> Taxon = 9593; gene = GGO106; Accession DDBJ/EMBL/GenBank = AF179755

<400> 218

Val Ala Ile Arg Lys Pro Leu His Tyr Leu Val Ile Met Arg Gln Trp
1 5 10 15

Val Cys Val Val Leu Leu Val Met Ser Trp Val Gly Gly Phe Leu His
20 25 30

Ser Val Phe Gln Leu Ser Ile Ile Tyr Gly Leu Pro Phe Cys Gly Pro
35 40 45

Asn Val Ile Asp His Phe Phe Cys Asp Met Tyr Pro Leu Leu Lys Leu
50 55 60

Val Cys Thr Asp Thr His Val Ile Gly Leu Leu Val Val Thr Asn Gly
65 70 75 80

Gly Leu Ser Cys Thr Ile Val Phe Leu Leu Leu Ile Ser Tyr Gly
85 90 95

Val Ile Leu His Ser Leu Lys Lys Leu Ser Gln Lys Gly Arg Gln Lys
100 105 110

Ala Leu Ser Thr Cys Ser Ser His Ile Thr Val Val Val Phe Phe Phe
115 120 125

Val Pro Cys Ile Phe Met Tyr Ala Arg Pro Ala Arg Ser Phe Pro Ile
130 135 140

Asp Lys Ser Val Ser Val Phe Tyr Thr Val Ile Thr Pro Met
145 150 155

<210> 219

<211> 488

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 9593; gene = GGO107; Accession DDBJ/EMBL/GenBank = AF179756

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 219

t ctt gcc atc tgc tat cct tta cac tac gga gcc atg atg agt agc ctg 49
Leu Ala Ile Cys Tyr Pro Leu His Tyr Gly Ala Met Met Ser Ser Leu
1 5 10 15

ctc tca gtg cag ttg gcc ctg ggc tcc tgg gtt tgt ggt ttc atg gcc 97
Leu Ser Val Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Met Ala
20 25 30

att gca gtg ccc aca gcc ctc atc agt ggc ctg tcc ttc tgt ggc ccc 145
Ile Ala Val Pro Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Pro
35 40 45

cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg 193
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
50 55 60

gcc tgc acc aac aca cag gca gta gag ctt gtg gcc ttt gtg att gct 241
Ala Cys Thr Asn Thr Gln Ala Val Glu Leu Val Ala Phe Val Ile Ala
65 70 75 80

gtt	gtg	gtt	atc	ctg	agt	tca	tgc	ctc	atc	acc	ctt	gtc	tcc	tat	gtg	289
Val	Val	Val	Ile	Leu	Ser	Ser	Cys	Leu	Ile	Thr	Leu	Val	Ser	Tyr	Val	
			85						90					95		
tac	atc	atc	agc	acc	atc	ctc	agg	atc	ccc	tct	gcc	agt	ggc	cgg	agc	337
Tyr	Ile	Ile	Ser	Thr	Ile	Leu	Arg	Ile	Pro	Ser	Ala	Ser	Gly	Arg	Ser	
			100					105					110			
aaa	gcc	ttc	tcc	acg	tgc	tcc	tcg	cat	ctc	acc	gtg	gtg	ctc	att	tgg	385
Lys	Ala	Phe	Ser	Thr	Cys	Ser	Ser	His	Leu	Thr	Val	Val	Leu	Ile	Trp	
		115					120					125				
tat	ggg	tcc	aca	att	ttc	ctt	cac	gtc	cgc	acc	tct	atc	aaa	gac	gcc	433
Tyr	Gly	Ser	Thr	Ile	Phe	Leu	His	Val	Arg	Thr	Ser	Ile	Lys	Asp	Ala	
	130					135					140					
ttg	gat	ctg	atc	aaa	gct	gtc	cac	gtc	ctg	aac	act	gtg	gtg	act	cca	481
Leu	Asp	Leu	Ile	Lys	Ala	Val	His	Val	Leu	Asn	Thr	Val	Val	Thr	Pro	
145					150					155					160	
gtt	tta	a														488
Val	Leu															
<210>	220															
<211>	162															
<212>	PRT															
<213>	Gorilla gorilla															
<220>																
<221>	misc_feature															
<222>	(1)..(488)															
<223>	Taxon = 9593; gene = GGO107; Accession DDBJ/EMBL/GenBank = AF179756															
<400>	220															
Leu	Ala	Ile	Cys	Tyr	Pro	Leu	His	Tyr	Gly	Ala	Met	Met	Ser	Ser	Leu	
1				5					10					15		
Leu	Ser	Val	Gln	Leu	Ala	Leu	Gly	Ser	Trp	Val	Cys	Gly	Phe	Met	Ala	
			20					25					30			
Ile	Ala	Val	Pro	Thr	Ala	Leu	Ile	Ser	Gly	Leu	Ser	Phe	Cys	Gly	Pro	
		35					40					45				
Arg	Ala	Ile	Asn	His	Phe	Phe	Cys	Asp	Ile	Ala	Pro	Trp	Ile	Ala	Leu	
	50					55					60					
Ala	Cys	Thr	Asn	Thr	Gln	Ala	Val	Glu	Leu	Val	Ala	Phe	Val	Ile	Ala	
65					70					75					80	
Val	Val	Val	Ile	Leu	Ser	Ser	Cys	Leu	Ile	Thr	Leu	Val	Ser	Tyr	Val	
				85					90					95		
Tyr	Ile	Ile	Ser	Thr	Ile	Leu	Arg	Ile	Pro	Ser	Ala	Ser	Gly	Arg		

115

120

125

Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Lys Asp Ala
130 135 140

Leu Asp Leu Ile Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
145 150 155 160

Val Leu

<210> 221

<211> 480

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(480)

<223> Taxon = 9593; gene = GGO108; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179757

<400> 221

tgtggcgggtg tgtaaccctc ttctctacac agttgcaatg tcccagaggc tttgctcctt 60

gttggtggct acatcatact gttgggggac agtctgttcc ctgacaccta ctttctactg 120

gaattatcct tcagaggaaa taatatcatt aataactttg tctgtgagca cgctgtcatt 180

gttgctgtgt cttgctctga cccctatttg agccaggaga tcactttagt ttctgccaac 240

attcaatgaa ataagcagcc tggatgatcat tctcacttcc tatgctttca tttttatcac 300

tgtcatgaag acgccttcca ctggggggcg caagaaagcg ttctccacgt gtgcctccca 360

cttgacggcc attaccattt tccatgggac tatccttttc ctctactgtg ttccctaactc 420

aagttcgcgg ctcatgggtca aggtggcctc tgtcttttgc acagtgggtca ttcccatgtg 480

<210> 222

<211> 487

<212> DNA

<213> Gorilla gorilla

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9593; gene = GGO109; Accession DDBJ/EMBL/GenBank = AF179758

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 222

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cac agc 49

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys


```

                20                25                30
gct ctt ttg cat acc ctc ctc ctg gcc cgg ctt tcc ttc tgt gct gac      145
Ala Leu Leu His Thr Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
      35                40                45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg      193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
      50                55                60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga      241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
      65                70                75                80

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt      289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
      85                90                95

cac att ggg gtc acc atc ctc cag att ccc tct acc aag ggc ata tgc      337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
      100                105                110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
      115                120                125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
      130                135                140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc      481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
      145                150                155                160

atg ttg      487
Met Leu

<210> 223
<211> 162
<212> PRT
<213> Gorilla gorilla

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9593; gene = GGO109; Accession DDBJ/EMBL/GenBank = AF179758

<400> 223

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser His Ser
1                5                10                15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
      20                25                30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
      35                40                45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
      50                55                60

```

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 224
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA1; Accession DDBJ/EMBL/GenBank = AF179759

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 224
t gta gcc ata tgt aat ccc ttg ctt tat cca gtg atg atg tcc aac aaa 49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Pro Val Met Met Ser Asn Lys
1 5 10 15

ctc agc gct cag ttg cta agt att tca tat gta att ggt ttc ctg cat 97
Leu Ser Ala Gln Leu Leu Ser Ile Ser Tyr Val Ile Gly Phe Leu His
20 25 30

cct ctg gtt cat gtg agt tta cta ttg cga cta act ttc tgc agg ttt 145
Pro Leu Val His Val Ser Leu Leu Leu Arg Leu Thr Phe Cys Arg Phe
35 40 45

aac ata ata cat tat ttc tac tgt gaa att tta caa ctg ttc aaa att 193
Asn Ile Ile His Tyr Phe Tyr Cys Glu Ile Leu Gln Leu Phe Lys Ile
50 55 60

tca tgc aat ggt cca tct att aac gca cta ata ata ttt att ttt ggt 241
Ser Cys Asn Gly Pro Ser Ile Asn Ala Leu Ile Ile Phe Ile Phe Gly
65 70 75 80

gct ttt ata caa ata ccc act tta atg act atc ata atc tct tat act 289

Tyr Gly Thr Leu Ile Phe Met Tyr Val Arg Pro Ala Ser Gly Leu Ala
 130 135 140

Glu Asp Gln Asp Lys Val Tyr Ser Leu Phe Tyr Thr Ile Ile Ile Pro
 145 150 155 160

Leu Leu

<210> 226
 <211> 487
 <212> DNA
 <213> Homo sapiens
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9606; gene = HSA10; Accession DDBJ/EMBL/GenBank = AF179760

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 226
 t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag 49
 Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
 1 5 10 15
 ctc tgt gtc ttc tta gtg gct gta tct cgg att ctg tct tgt gcc agc 97
 Leu Cys Val Phe Leu Val Ala Val Ser Arg Ile Leu Ser Cys Ala Ser
 20 25 30
 tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg 145
 Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45
 aac acc gtc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
 Asn Thr Val Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60
 tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
 Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80
 gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
 Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95
 tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac 337
 Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
 100 105 110
 aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat 385
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
 115 120 125
 tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct 433
 Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

<211> 487
 <212> DNA
 <213> Homo sapiens

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9606; gene = HSA12; Accession DDBJ/EMBL/GenBank = AF179761

 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 228
 t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

 ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97
 Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

 gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145
 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
 35 40 45

 aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193
 Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60

 gcc ttc tct gac act cga gtt aat gaa tgg gtg ata ttt atc atg gga 241
 Ala Phe Ser Asp Thr Arg Val Asn Glu Trp Val Ile Phe Ile Met Gly
 65 70 75 80

 ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca 289
 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
 85 90 95

 aga att gtc tcc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc 337
 Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110

 aag gcc ctc tct act tgt ggc tcc cac ctg tct gtg gtg tca ctg ttc 385
 Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

 tat gga acc gtt att ggt ctc tac tta tgc tca tca gct aat agt tct 433
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Ser Ser Ala Asn Ser Ser
 130 135 140

 act cta aag gac act gtc atg gct atg atg tac act gtg gtg acc ccc 481
 Thr Leu Lys Asp Thr Val Met Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

 atg ctg 487
 Met Leu

<210> 229
 <211> 162
 <212> PRT
 <213> Homo sapiens

 <220>


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cttctctatc tccttctcta agtccaacca tgtagacttc ttttctgtg acctcccacc 180
cctgctgaag cttgcctgta gtgaaaccag gccacgggaa tgggtgatct acctctcagc 240
tttctgggtc atcacaacca gcatttcagt gattcttaca tcgtacttgt tcatcattca 300
gtctattctg aagattcgta cagcagggtg aaagccaaga cttctccac ctgtgcttct 360
cacaagactg cattgactct cttctttgga acactcatat tcatatacct gaaaggcaac 420
atgggcgaat cccttgagga agacaagatc gtgtcaatat ttacactgt ggtcatcccc 480
atgcta 486

```

```

<210> 231
<211> 487
<212> DNA
<213> Homo sapiens

```

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<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA16; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179763

```

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<400> 231
catggccatt gtgaaccctt tactttatac agtagctatg actaaaatag tttgtattgt 60
gctcgcattt gggcatgta tgggaggtt aatcagctca ttgacacata caattggctt 120
ggtgaaaactg tcttctgtg ggccaaatgt catcagtcac ttcttctgtg atcttcccc 180
actgttgaag ctgtcatgtt ctgagacatc tatgaatgaa ttgttgcttt tgatcttctc 240
tggcattatt gccacgctca cttttttgac tgtggtgatc tcctacatct tcattgttgc 300
tgctatcctg aggatccgct aagaagcagg tagacgtaaa gccttctcca cctgcacctc 360
tcacctgatt accgtgacct tattctatgg atcgataagc tttagttaca ttcagccaaa 420
ctcccagtat tccctagaac aagaaaaggt ggtgtctgta tttataccc tgggtggtcc 480
tatgtta 487

```

```

<210> 232
<211> 485
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 9606; gene = HSA18; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179764

```

```

<400> 232
cgtgggcac tgtaaccac tgtgttacac ggtcaccatg tctccccaga agtgtttgct 60
ccttttactg ggtgtctatg ggatggggat tttggggctg tggctcatat gggaaacata 120
atgtttatgt ctttttgtg agacaacctt gtcaatcaat atatgtgtga catccttctc 180
ctccttgagc tctcctgcaa cagctcttac ataaatttgc tgggtggtttt tattattgtg 240

```



```
accgttggca ttgggggtgcc gattgtcacc atttttctct cttatgggtt tattctttcc 300
agcattctcc acattagttc cacagagggc aggtctaaag ccttcagtag ctgcagttcc 360
cacataattg tggtagcgct ttctttgggt caggtgcttt catgtacctc aaaccacctt 420
ctattctacc cctggaccag gggaaagtgt cctccatttt ttgtactgct gtggtgcccc 480
tgttt 485
```

```
<210> 233
<211> 486
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9606; gene = HSA2; pseudogene; Accession DDBJ/EMBL/GenBank =
AF179765
```

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<400> 233
cgtgggcac tgtaaccac tgtgtacac ggtcaccatg tctcccaga tgtgtttgct 60
ccttttactg ggtgtctatg ggggtgggat tttgggctg tggctcatat gggaaacata 120
atgtttatgt ccttttgtgg agacaacctt gtcaatcact atatgtgtga catccttcc 180
ctccttgagc cctcctgcaa cagctcttac ataaatttgc tgggtggtttt tattattgtg 240
accgttggca ttgggggtgcc gattgtcacc atttttctct cttatgggtt tattctttcc 300
agcattctcc acattagttc cacagagggc aggtctaaag ccttcagtag ctgcagttcc 360
cacataattg tggtagcgct tttctttggg tcaggtgctt tcatgtacct caaaccacct 420
tctattctac ccctggacca ggggaaagtg tctccatttt tttgtactgc tgtggtgccc 480
atgttt 486
```

```
<210> 234
<211> 487
<212> DNA
<213> Homo sapiens
```

```
<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA3; Accession DDBJ/EMBL/GenBank = AF179766
```

```
<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor
```

```
<400> 234
t gtg gcc atc tgt aaa ccc ctt cat tat gtg gtc atc atg aac aac agg 49
Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
1 5 10 15

gtg tgt acc tta tta gtt ctc tgc tgt tgg gtg gct ggc ttg atg atc 97
Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
20 25 30
```

```

att gtt cca cca ctt agc tta ggc ctc cag ctc gaa ttc tgt gac tcc      145
Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
      35              40              45

aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc      193
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
      50              55              60

tca tgc tca gat aca tgg gta ata gaa cag atg gtt ata ctt atg gct      241
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
      65              70              75              80

gta ttt gca ctc att atc acc cca gtt tgt gtg att ctg tcc tac ttg      289
Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
      85              90              95

tac ata gtc aga aca att ctg aag ttc cct tct gtt cag caa agg aaa      337
Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
      100             105             110

aag gcc ttt tct acc tgt tca tcc cac atg att gtg gtt tcc att gcc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
      115             120             125

tat gga agc tgc atc ttc atc tat atc aag ccc tct gca aaa gat gag      433
Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
      130             135             140

gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtc gca ccc      481
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
      145             150             155             160

ttg ttg
Leu Leu
      487

```

```

<210> 235
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA3; Accession DDBJ/EMBL/GenBank = AF179766

<400> 235

```

```

Val Ala Ile Cys Lys Pro Leu His Tyr Val Val Ile Met Asn Asn Arg
1              5              10              15

```

```

Val Cys Thr Leu Leu Val Leu Cys Cys Trp Val Ala Gly Leu Met Ile
      20              25              30

```

```

Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Asp Ser
      35              40              45

```

```

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
      50              55              60

```

Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Met Val Ile Leu Met Ala
65 70 75 80

Val Phe Ala Leu Ile Ile Thr Pro Val Cys Val Ile Leu Ser Tyr Leu
85 90 95

Tyr Ile Val Arg Thr Ile Leu Lys Phe Pro Ser Val Gln Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
115 120 125

Tyr Gly Ser Cys Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Asp Glu
130 135 140

Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
145 150 155 160

Leu Leu

<210> 236
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA5; Accession DDBJ/EMBL/GenBank = AF179767

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 236
t gtt gcc ata tgt cac cct ctc cac tac act gtc atc atg agg gaa gag 49
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1 5 10 15

ctc tgt gtc ttc tta gtg gct gta act tgg att ctg tct tgt gcc agc 97
Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
20 25 30

tcc ctc tct cac acc ctt ctc ctg acc cgg ctg tct ttc tgt gct gcg 145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
35 40 45

aac acc atc ccc cat gtc ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg 241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly

```

      85              90              95
tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cac      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100              105              110

aaa gca ttg tcc aca tgt ggc tcc cat ctc tct gtg gtg tct ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115              120              125

tat ggg tca ata ttt ggc cag tac ctt ttc ccg act gta agc agt tct      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
      130              135              140

att gac aag gat gtc att gtg gct ctc atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
      145              150              155              160

atg ttg      487
Met Leu

```

```

<210> 237
<211> 162
<212> PRT
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA5; Accession DDBJ/EMBL/GenBank = AF179767

<400> 237

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```

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Ile Met Arg Glu Glu
1              5              10              15

```

```

Leu Cys Val Phe Leu Val Ala Val Thr Trp Ile Leu Ser Cys Ala Ser
      20              25              30

```

```

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35              40              45

```

```

Asn Thr Ile Pro His Val Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50              55              60

```

```

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65              70              75              80

```

```

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
      85              90              95

```

```

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile His
      100              105              110

```

```

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115              120              125

```

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 238
 <211> 478
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(478)
 <223> Taxon = 9606; gene = HSA6; pseudogene; Accession DDBJ/EMBL/GenBank = AF179768

<400> 238
 tgttgccatc tgtaaccctt tgcgctacct tacagtcattg aacccccagc tatgcctttg 60
 gttgggttctt gcctgctggt gtggggggttt tatccactct atcatgcagg tcataactagt 120
 catccagctg cctttctgtg ggcccaatga actggacaac ttctactgtg atgtcctaca 180
 aatcatcaag ctggcctgca tggacacctt tgtggttagag gtgctggtga tagccaacag 240
 tggctctgctg tctcttctgt gcttcttgggt cttactattc tcttatgcta tcatcctgat 300
 caccctgaga acacgcttct gccagggcca gaacaaggct ctctctacct gtgcttctca 360
 cctgacagtg gtcagcctga tcttcgtgcc atgcgtattc atctatttga ggcccttctg 420
 cagcttctct gtggataaga tattctcctt gttttacaca gtgattacac ctatgttg 478

<210> 239
 <211> 488
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(488)
 <223> Taxon = 9606; gene = HSA7; pseudogene; Accession DDBJ/EMBL/GenBank = AF179769

<400> 239
 catggccatc tgcaagccct tggttatatg aagcaaatg accaggtgtg tctgcctctg 60
 tctggctgct gctccctata tttatggctt tgcaaatggt ctaagcacag accaccctga 120
 tgcttctgt gtccttctgt ggacccaatg acatcaacca cttttactgt gcggaccac 180
 ccctcttagt cctcgctgct tcagatactt atgtcaaaga gaccgcatg ttggtggtgg 240
 ctggttccaa cctcatttgc tctctcaccg tcatcctcat ttctacact ttcattctca 300
 ctgccattct gcgtatccac actgctgagg ggaggcgcaa ggccttctcc acctgctggg 360

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ctcatgtgac cgctgtcact gtcttctatg ggacactgtt ctgcatgtac ctgaggcccc 420
cttctgagac atctatacaa caggggaaaa ttgtagctgt tttttatata tttgtgagtc 480
cgatgtta 488

<210> 240
<211> 487
<212> DNA
<213> Homo sapiens

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9606; gene = HSA8; Accession DDBJ/EMBL/GenBank = AF179770

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 240
t gtt gcc atc tgc aag ccc ctt cat tac aca tcc atc atg aac agg aaa 49
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
1 5 10 15

ctc tgc act cta ctt gtg ctg tgt gcc tgg cta agt ggg ttt ctg acc 97
Leu Cys Thr Leu Leu Val Leu Cys Ala Trp Leu Ser Gly Phe Leu Thr
20 25 30

att ttc cca ccc ctt atg ctt ctc ctc cag ctg gat tac tgt gct tcc 145
Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser
35 40 45

aac gtc att gat cac ttt gca tgt gac tat ttt ccc ctc tta caa cta 193
Asn Val Ile Asp His Phe Ala Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50 55 60

tct tgt tca gat aca tgg ctc cta gaa gta att ggt ttt tac ttt gct 241
Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
65 70 75 80

ttg gtt act ttg ctg ttc act ttg gca tta gtg att tta tct tac atg 289
Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
85 90 95

tac att atc agg acc att ttg aga atc ccg tct gcc agt caa aga aaa 337
Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
100 105 110

aag gct ttc tcc act tgt tct tct cac atg att gtc att tcc att tct 385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

tat gga agc tgt ata ttc atg tat gct aat cca tct gca aaa gaa aag 433
Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
130 135 140

gca tca ttg aca aaa gga ata gct att ctc aat aca tct gtt gcc ccc 481
Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
145 150 155 160

atg ctg 487
Met Leu

```

Table 1. Demographic characteristics of the study population	
Age (years)	18-24, 25-34, 35-44, 45-54, 55-64, 65-74, 75-84, 85-94
Gender	Male, Female
Ethnicity	White, Black, Hispanic, Asian, Other
Education	Less than high school, High school, Some college, College, Graduate
Income	Less than \$10,000, \$10,000-\$19,999, \$20,000-\$29,999, \$30,000-\$39,999, \$40,000-\$49,999, \$50,000-\$59,999, \$60,000-\$69,999, \$70,000-\$79,999, \$80,000-\$89,999, \$90,000-\$99,999, \$100,000+
Marital status	Married, Divorced, Widowed, Single
Health insurance	Medicaid, Medicare, Private, Other
Employment	Employed, Unemployed, Retired
Health status	Good, Fair, Poor
Chronic conditions	Hypertension, Diabetes, Heart disease, Asthma, Cancer, Other
Medication use	Yes, No
Healthcare utilization	Regular, Irregular, No
Healthcare satisfaction	Satisfied, Dissatisfied
Healthcare access	Easy, Difficult
Healthcare quality	High, Low
Healthcare cost	Low, High
Healthcare coverage	Full, Partial, None
Healthcare utilization (continued)	Frequency, Duration, Location
Healthcare satisfaction (continued)	Quality of care, Access to care, Cost of care
Healthcare access (continued)	Distance to care, Transportation, Hours of operation
Healthcare quality (continued)	Staffing, Facilities, Equipment, Services
Healthcare cost (continued)	Insurance premiums, Out-of-pocket costs, Hidden costs
Healthcare coverage (continued)	Types of services covered, Limits on coverage, Exclusions
Healthcare utilization (continued)	Prevalence of use, Incidence of use, Remission of use
Healthcare satisfaction (continued)	Patient satisfaction, Provider satisfaction, System satisfaction
Healthcare access (continued)	Physical access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs, Gross costs, Total costs
Healthcare coverage (continued)	Public coverage, Private coverage, Government coverage
Healthcare utilization (continued)	Unnecessary use, Appropriate use, Underuse
Healthcare satisfaction (continued)	Perceived quality, Actual quality, Expected quality
Healthcare access (continued)	Geographic access, Financial access, Informational access
Healthcare quality (continued)	Structural quality, Process quality, Outcome quality
Healthcare cost (continued)	Direct costs, Indirect costs, Intangible costs
Healthcare coverage (continued)	Essential health benefits, Community rating, Risk adjustment
Healthcare utilization (continued)	Primary care, Specialty care, Hospital care, Long-term care
Healthcare satisfaction (continued)	Communication, Continuity of care, Coordination of care
Healthcare access (continued)	Language barriers, Cultural barriers, Health literacy
Healthcare quality (continued)	Accreditation, Certification, Accreditation by specialty
Healthcare cost (continued)	Net costs,

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Ser Ile Met Asn Arg Lys
1 5 10 15

Ile Phe Pro Pro Leu Met Leu Leu Leu Gln Leu Asp Tyr Cys Ala Ser
35 40 45

Ser Cys Ser Asp Thr Trp Leu Leu Glu Val Ile Gly Phe Tyr Phe Ala
65 70 75 80

Leu Val Thr Leu Leu Phe Thr Leu Ala Leu Val Ile Leu Ser Tyr Met
85 90 95

Tyr Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Ala Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ala Asn Pro Ser Ala Lys Glu Lys
130 135 140

Ala Ser Leu Thr Lys Gly Ile Ala Ile Leu Asn Thr Ser Val Ala Pro
145 150 155 160

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<210> 242
<211> 485
<212> DNA
<213> Eulemur fulvus
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210

<223> Taxon = 13515; gene = EFU145; Accession DDBJ/EMBL/GenBank = AF179771

<220>

<221> CDS

<222> (2)..(484)

<223> Product = olfactory receptor

<400> 242

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t gtg gcc atc tgc cag cca ctc caa tac agc aca gct atg agt cac cag      49
  Val Ala Ile Cys Gln Pro Leu Gln Tyr Ser Thr Ala Met Ser His Gln
    1              5              10              15

ctc tgt gca ctc atg ctg gcc atg tgc tgg ctg cta acc aac tgt cct      97
Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
      20              25              30

gca ttg atg cac acg ctg ttg ctg acc cgt gtg gct ttc tgt gcc cag      145
Ala Leu Met His Thr Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
      35              40              45

agg gcc atc ccc cac ttc tac tgt gat ccc agt gct ctc ctg aag ctc      193
Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
      50              55              60

gcc tgc tcg gat acc cgc ata aac gag ctg atg atc atc gcc atg ggc      241
Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
      65              70              75              80

ttg gcc ttc ctc acg gtt ccc ctc acg ctg atc gtc ttc tcc tac gtc      289
Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
      85              90              95

cgc atc tcc tgg gct gtg ctt ggc atc tcg tct cct gga ggg cga tgc      337
Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
      100              105              110

aaa gcc ttc tcc acc tgt ggt tct cat ctc acg gtg gtt ctg ctc ttc      385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
      115              120              125

tat ggg tct ctt atg ggt gtg tat ttg ctt cct ccg tca tct tac tct      433
Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
      130              135              140

aca gag agg gaa agc agg gct gcc att ctc tac atg gtg atc att ccc      481
Thr Glu Arg Glu Ser Arg Ala Ala Ile Leu Tyr Met Val Ile Ile Pro
      145              150              155              160

atg t                                                                485
Met
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<210> 243

<211> 161

<212> PRT

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 13515; gene = EFU145; Accession DDBJ/EMBL/GenBank = AF179771

<400> 243

Val Ala Ile Cys Gln Pro Leu Gln Tyr Ser Thr Ala Met Ser His Gln

EFU146" 59724260

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1           5           10           15

Leu Cys Ala Leu Met Leu Ala Met Cys Trp Leu Leu Thr Asn Cys Pro
      20           25           30

Ala Leu Met His Thr Leu Leu Leu Thr Arg Val Ala Phe Cys Ala Gln
      35           40           45

Arg Ala Ile Pro His Phe Tyr Cys Asp Pro Ser Ala Leu Leu Lys Leu
      50           55           60

Ala Cys Ser Asp Thr Arg Ile Asn Glu Leu Met Ile Ile Ala Met Gly
      65           70           75           80

Leu Ala Phe Leu Thr Val Pro Leu Thr Leu Ile Val Phe Ser Tyr Val
      85           90           95

Arg Ile Ser Trp Ala Val Leu Gly Ile Ser Ser Pro Gly Gly Arg Cys
      100          105          110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Val Val Leu Leu Phe
      115          120          125

Tyr Gly Ser Leu Met Gly Val Tyr Leu Leu Pro Pro Ser Ser Tyr Ser
      130          135          140

Thr Glu Arg Glu Ser Arg Ala Ala Ile Leu Tyr Met Val Ile Ile Pro
      145          150          155          160

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Met

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<210> 244
<211> 485
<212> DNA
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(485)
<223> Taxon = 13515; gene = EFU146; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179772

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<400> 244
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gctcatcctc gcctgctggc tggcagggtt ctcttcacac attgtgcctg tcatcctgac      120
cagtcagctt ccattctgtg acaccacat caaccacttc ttctgtgact atacacctct      180
aatggagggtg gtctgcagtg ggccaaaggt gctggagatg gtggatttta ccctggcctt      240
ggtggcaccg ctcagcacct tgggtgctgat caccctgtcc tacatccaga tcatcagcac      300
gattgtcagg atcccctctg tccaggagag gaaaaaggct ttctccacct gttcctccca      360

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tgtcatcgtg gttaccatgt gctatggaaa gctgtttttt tatgtatgtc aagccctccc      420
caggcaaagg ggttgatcta aacaaaggag tgtctctaata caatacagtt attgcccccc      480
tcttg                                             485

<210> 245
<211> 487
<212> DNA
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU147; Accession DDBJ/EMBL/GenBank = AF179773

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 245
c  gtg gcc atc tgc ctt cct ctg cac tac acc atg gtc atg aaa ccc cga      49
   Val Ala Ile Cys Leu Pro Leu His Tyr Thr Met Val Met Lys Pro Arg
   1             5             10             15

tgc tgc ctg atg ctg gtg gca gca tcc tgg ctc tgc tcc cac tgc ctg      97
Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
             20             25             30

gct ttc tct ctc acc ctt ctg atg act cag ttc tca ttc tgt gcc tcc      145
Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
             35             40             45

cat tcc atc caa cac ttt ttc tgt gat gta ccc cca ctc ctc aaa ctt      193
His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
             50             55             60

gcc tgt tca gac acc cat atc ttt cag gtc aca atg tta act gaa gga      241
Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
             65             70             75             80

gtc ctc tca ggt gtg atc cct ctt acc tgt gtc ctg gtc tct tat gcc      289
Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
             85             90             95

cac atc atg cac acc atc ctc agg atc cct tct gct ggg ggc aag cac      337
His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
             100            105            110

aaa gtc ttc tct acc tgt ggc tct cac ctg tca gtg gtc act ctc ttc      385
Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe
             115            120            125

tat ggg acc ctc ttt ctg gtg tat ttc cag cct tca tcc tcc tac tca      433
Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
             130            135            140

gca gat act gga atg gtg gca tgt gta gta tac acg atg gtc acc ccc      481
Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
             145            150            155            160

atg gtg                                             487
Met Val

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<210> 246
 <211> 162
 <212> PRT
 <213> Eulemur fulvus

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 13515; gene = EFU147; Accession DDBJ/EMBL/GenBank = AF179773

 <400> 246

Val Ala Ile Cys Leu Pro Leu His Tyr Thr Met Val Met Lys Pro Arg
 1 5 10 15

Cys Cys Leu Met Leu Val Ala Ala Ser Trp Leu Cys Ser His Cys Leu
 20 25 30

Ala Phe Ser Leu Thr Leu Leu Met Thr Gln Phe Ser Phe Cys Ala Ser
 35 40 45

His Ser Ile Gln His Phe Phe Cys Asp Val Pro Pro Leu Leu Lys Leu
 50 55 60

Ala Cys Ser Asp Thr His Ile Phe Gln Val Thr Met Leu Thr Glu Gly
 65 70 75 80

Val Leu Ser Gly Val Ile Pro Leu Thr Cys Val Leu Val Ser Tyr Ala
 85 90 95

His Ile Met His Thr Ile Leu Arg Ile Pro Ser Ala Gly Gly Lys His
 100 105 110

Lys Val Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Leu Phe
 115 120 125

Tyr Gly Thr Leu Phe Leu Val Tyr Phe Gln Pro Ser Ser Ser Tyr Ser
 130 135 140

Ala Asp Thr Gly Met Val Ala Cys Val Val Tyr Thr Met Val Thr Pro
 145 150 155 160

Met Val

<210> 247
 <211> 487
 <212> DNA
 <213> Eulemur fulvus

<220>
 <221> misc_feature

09747155.000001

<222> (1)..(487)
 <223> Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 247
 t gtg gcc atc tgc aaa ccg ctg cat tat gtg gcc att atg agt aac aca 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
 1 5 10 15
 gtc tgc aga aga ctt gtc ttt tgt tgt tgg gta gct ggt ctg ttt att 97
 Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
 20 25 30
 ata atc cct cca ctt agc ctg ggc cta aat ctg gaa ttt tgt gat tct 145
 Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser
 35 40 45
 gat acc att gat cat ttt atc tgt gat gca tct ccc ctc ctg aat atc 193
 Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile
 50 55 60
 tct tgt tca aat act tgg ttc atg gaa cag act gtt atc atc tgt gca 241
 Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala
 65 70 75 80
 gtg ctg acc ctc att atg aca ctt atg tgt gta gtt ctg tcc tac att 289
 Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile
 85 90 95
 tat atc atc aag aca att tta gga ttc tct tct gcc cag caa aag aaa 337
 Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys
 100 105 110
 aaa gcc ttt tcc acc tgt tct tcc cac atg att gtg gtg tcc atc acc 385
 Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr
 115 120 125
 tat ggc agc tac atc ttc atc tat atc aaa cct tct gca aag gaa gaa 433
 Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu
 130 135 140
 gta gcc att aac aag ggt gtg aca gtc ctc act act tcc atc gcc ccc 481
 Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro
 145 150 155 160
 atg ctg 487
 Met Leu

<210> 248
 <211> 162
 <212> PRT
 <213> Eulemur fulvus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 13515; gene = EFU148; Accession DDBJ/EMBL/GenBank = AF179774
 <400> 248

Val Ala Ile Cys Lys Pro Leu His Tyr Val Ala Ile Met Ser Asn Thr
 1 5 10 15

Val Cys Arg Arg Leu Val Phe Cys Cys Trp Val Ala Gly Leu Phe Ile
 20 25 30

Ile Ile Pro Pro Leu Ser Leu Gly Leu Asn Leu Glu Phe Cys Asp Ser
 35 40 45

Asp Thr Ile Asp His Phe Ile Cys Asp Ala Ser Pro Leu Leu Asn Ile
 50 55 60

Ser Cys Ser Asn Thr Trp Phe Met Glu Gln Thr Val Ile Ile Cys Ala
 65 70 75 80

Val Leu Thr Leu Ile Met Thr Leu Met Cys Val Val Leu Ser Tyr Ile
 85 90 95

Tyr Ile Ile Lys Thr Ile Leu Gly Phe Ser Ser Ala Gln Gln Lys Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Thr
 115 120 125

Tyr Gly Ser Tyr Ile Phe Ile Tyr Ile Lys Pro Ser Ala Lys Glu Glu
 130 135 140

Val Ala Ile Asn Lys Gly Val Thr Val Leu Thr Thr Ser Ile Ala Pro
 145 150 155 160

Met Leu

<210> 249
 <211> 487
 <212> DNA
 <213> Eulemur fulvus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 249
 t gtt gct atc tgt aag ccc ctg cat tac agg gtc atc atg aat cga aga 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
 1 5 10 15

gtc tgc aca ctg ctc gtc ttt gcc tct tgg ctg gtt tca ttc tta atc 97
 Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile

```

20          25          30
gta ttc cca gca ctc atg ttg ctc tta aag ctt gat tac tgt gga ttt      145
Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe
      35          40          45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt      193
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
      50          55          60

tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct      241
Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
      65          70          75          80

gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg      289
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met
      85          90          95

cac atc gtg aga acg att ttg aga att cct tct act agt cag agg aca      337
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
      100          105          110

aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
      115          120          125

tat ggc agc tgc att ttt atg tac att aag ccc tca gca aag gat aga      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
      130          135          140

gta tct ttg agc aag gca gtg gct gtg cta atc acc tca gta gct ccc      481
Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
      145          150          155          160

atg ctc      487
Met Leu

<210> 250
<211> 162
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU149; Accession DDBJ/EMBL/GenBank = AF179775

<400> 250

Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
1          5          10          15

Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
20          25          30

Val Phe Pro Ala Leu Met Leu Leu Leu Lys Leu Asp Tyr Cys Gly Phe
35          40          45

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
50          55          60

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<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 252
t ctg gct atc tgc tat cct cta cac tac agg aca atc atg agc agc ctg      49
  Leu Ala Ile Cys Tyr Pro Leu His Tyr Arg Thr Ile Met Ser Ser Leu
    1             5             10             15

ctg gct aca cag ctg gcc ttg ggc tcc tgg gtc tgt ggt ttc ctg gcc      97
Leu Ala Thr Gln Leu Ala Leu Gly Ser Trp Val Cys Gly Phe Leu Ala
    20             25             30

att gca gtg ctg acg gcc ctt atc agt ggc ctg tcc ttc tgt ggc gcc      145
Ile Ala Val Leu Thr Ala Leu Ile Ser Gly Leu Ser Phe Cys Gly Ala
    35             40             45

cgt gcc atc aac cac ttc ttc tgt gac att gca ccc tgg att gcc ctg      193
Arg Ala Ile Asn His Phe Phe Cys Asp Ile Ala Pro Trp Ile Ala Leu
    50             55             60

gcc tgc acc agc aca cag gca ata gag ctc gtg gcc ttt gtg att gct      241
Ala Cys Thr Ser Thr Gln Ala Ile Glu Leu Val Ala Phe Val Ile Ala
    65             70             75             80

ttt gtg gtc atc ctg agt tca tgc ctc atc acc ctg gtc tcc tac gtg      289
Phe Val Val Ile Leu Ser Ser Cys Leu Ile Thr Leu Val Ser Tyr Val
    85             90             95

tac att atc agc acc atc ctc agg atc cca tct gcc agc ggc cgg agc      337
Tyr Ile Ile Ser Thr Ile Leu Arg Ile Pro Ser Ala Ser Gly Arg Ser
    100            105            110

aaa gcc ttc tct acg tgc tcc tct cac ctc acc gtg gtg ctc atc tgg      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Thr Val Val Leu Ile Trp
    115            120            125

tat ggg tcc acg att ttt ctt cat gtc cgc acc tcc atc aca gac gcc      433
Tyr Gly Ser Thr Ile Phe Leu His Val Arg Thr Ser Ile Thr Asp Ala
    130            135            140

ttg gat ctg acc aaa gct gtc cat gtc ctg aac acc gtg gtg act cca      481
Leu Asp Leu Thr Lys Ala Val His Val Leu Asn Thr Val Val Thr Pro
    145            150            155            160

gtt cta
Val Leu      487

<210> 253
<211> 162
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU151; Accession DDBJ/EMBL/GenBank = AF179777

<400> 253

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Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
      20                      25                      30

gta ttc cca gca ctc atg ttg ctg tta aag ctt gat tac tgt gga ttt      145
Val Phe Pro Ala Leu Met Leu Leu Lys Leu Asp Tyr Cys Gly Phe
      35                      40                      45

aat att att gac cat ttt acc tgt gat tat ttt ccc ctg ctg cag ctt      193
Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
      50                      55                      60

tcc tgt tca gat aca aaa ttc ctg gag ata atg ggg ttt tcc tgt gct      241
Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
      65                      70                      75                      80

gtg ttt act cta atg ttc act ttg gca tta ata ttt ctg tcc tac atg      289
Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met
      85                      90                      95

cac atc gtg agg acg att ttg aga att cct tct act agt cag agg aca      337
His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
      100                      105                      110

aag gcc ttt tct aca tgt tct tcc cac atg att gtc atc tcc atc tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
      115                      120                      125

tat ggc agc tgc att ttt atg tac att aag ccc tca gca aaa gat aga      433
Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
      130                      135                      140

gta tct ttg agc aag gca gtg gct gtg cta atc acc tca gta gct ccc      481
Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
      145                      150                      155                      160

atg ctc      487
Met Leu

```

```

<210> 255
<211> 162
<212> PRT
<213> Eulemur fulvus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 13515; gene = EFU153; Accession DDBJ/EMBL/GenBank = AF179778

<400> 255

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Val Ala Ile Cys Lys Pro Leu His Tyr Arg Val Ile Met Asn Arg Arg
1                      5                      10                      15

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Val Cys Thr Leu Leu Val Phe Ala Ser Trp Leu Val Ser Phe Leu Ile
      20                      25                      30

```

```

Val Phe Pro Ala Leu Met Leu Leu Lys Leu Asp Tyr Cys Gly Phe
      35                      40                      45

```

```

Asn Ile Ile Asp His Phe Thr Cys Asp Tyr Phe Pro Leu Leu Gln Leu
      50                      55                      60

```

Ser Cys Ser Asp Thr Lys Phe Leu Glu Ile Met Gly Phe Ser Cys Ala
65 70 75 80

Val Phe Thr Leu Met Phe Thr Leu Ala Leu Ile Phe Leu Ser Tyr Met
85 90 95

His Ile Val Arg Thr Ile Leu Arg Ile Pro Ser Thr Ser Gln Arg Thr
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Ile Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Ala Lys Asp Arg
130 135 140

Val Ser Leu Ser Lys Ala Val Ala Val Leu Ile Thr Ser Val Ala Pro
145 150 155 160

Met Leu

<210> 256

<211> 488

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 256

c atg gcc atc tgc cat ccg ctc cgt tac cct gtc ttc atg aac cac agg 49
Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg
1 5 10 15

gtg tgt ctc ttc ctg gca tct ggc tgc tgg ttc ctg gga tca gta gat 97
Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp
20 25 30

ggc ttc atg ctc act cca atc acc atg acc ttc ccc tac tgc agg tcc 145
Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser
35 40 45

cgg gag att cac cat tcc ttc tgc gaa gtc cct gct gta acg acg ctt 193
Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu
50 55 60

tcc tgc tca gac acc tca ctc tat gaa atg ctc atg tac ctg tgc tgt 241
Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys
65 70 75 80

```

gtc ctc atg ctc ctc att cct gtg aca gtc att tca agc tcc tat tca      289
Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser
                        85                        90                        95

ttc att ctc ctc acc atc cac agg atg ggc tca gca gag ggc cgg aag      337
Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys
                        100                        105                        110

aag gcc ttt gcc acc tgt tcc tcc cac atg acc gtg gtt atc ctc ttc      385
Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe
                        115                        120                        125

tat ggg gcc gcc atc tac acc tac atg ctc ccc agc tcc tac cac act      433
Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
                        130                        135                        140

cct gag aag gac atg atg gtg tct gtc ttt tat acc atc cta act cct      481
Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro
145                        150                        155                        160

gtg cta a                                                                488
Val Leu

```

```

<210> 257
<211> 162
<212> PRT
<213> Eulemur fulvus

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```

<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 13515; gene = EFU154; Accession DDBJ/EMBL/GenBank = AF179779

<400> 257

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Met Ala Ile Cys His Pro Leu Arg Tyr Pro Val Phe Met Asn His Arg
1                        5                        10                        15

```

```

Val Cys Leu Phe Leu Ala Ser Gly Cys Trp Phe Leu Gly Ser Val Asp
20                        25                        30

```

```

Gly Phe Met Leu Thr Pro Ile Thr Met Thr Phe Pro Tyr Cys Arg Ser
35                        40                        45

```

```

Arg Glu Ile His His Ser Phe Cys Glu Val Pro Ala Val Thr Thr Leu
50                        55                        60

```

```

Ser Cys Ser Asp Thr Ser Leu Tyr Glu Met Leu Met Tyr Leu Cys Cys
65                        70                        75                        80

```

```

Val Leu Met Leu Leu Ile Pro Val Thr Val Ile Ser Ser Ser Tyr Ser
85                        90                        95

```

```

Phe Ile Leu Leu Thr Ile His Arg Met Gly Ser Ala Glu Gly Arg Lys
100                        105                        110

```

```

Lys Ala Phe Ala Thr Cys Ser Ser His Met Thr Val Val Ile Leu Phe

```

115

120

125

Tyr Gly Ala Ala Ile Tyr Thr Tyr Met Leu Pro Ser Ser Tyr His Thr
 130 135 140

Pro Glu Lys Asp Met Met Val Ser Val Phe Tyr Thr Ile Leu Thr Pro
 145 150 155 160

Val Leu

<210> 258

<211> 488

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(488)

<223> Taxon = 13515; gene = EFU155; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179780

<400> 258

tgttgctatc tgtaagcccc tgcattacaa ggtcatcatg aatcgaagag tcgtgcacac 60

tgctcgtctt tgcctcttgg ctggtttcat tcttaatcgt attcccagca ctcatgttgc 120

tcttaaagct tgattactgt ggatttaata ttattgacca ttttacctgt gattattttc 180

ccttgctgca gctttcctgt tcagatacaa aattcctgga gataatgggg ttttcctgtg 240

ctgtgtttac tctaatgttc actttggcat taatatttct gtcctacatg cacatcgtga 300

gaacgatttt gagaattcct tctactagtc agaggacaaa ggccttttct acatgttctt 360

cccacatgat tgtcatctcc atctcttatg gcagctgcat ttttatgtac attaagccct 420

cagcaaagga tagagtatct ttgagcaagg cagtggctgt gctaatacacc tcagtagctc 480

ccatgcac 488

<210> 259

<211> 486

<212> DNA

<213> Eulemur fulvus

<220>

<221> misc_feature

<222> (1)..(486)

<223> Taxon = 13515; gene = EFU156; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179781

<400> 259

tgtggccatc tgcaagcccc tgcattatgt gacogtcatg aacagcagag tttgcaggat 60

tctcatcatc tgttggtggg tggtgggtt atgcataata atccctccac ttagcctggg 120

tttaaactta aaattctgtg actctaacat gattgatcat tttgggttgcg atgcatttcc 180

cctggtgaaa atctcatgct cagacacatg gttcatggaa cagacgggta tcatctgtgc 240

tgtgctgacc ctgaatatga ctctaacttg tgtagttctg tcatacgctt acatcatcaa 300
gacaatTTTT agattccctt ctgtccagca aaggaaaaag gccttttcca cctgttcttc 360
ccacatgatt gtgggtttcca tcacctatgg caggtgcatt ttcattctaca tgaatcctac 420
agcaaaggaa gaagtgaccg ttaataaagt agtttctttg ctcatttctt ctattttgct 480
acattg 486

<210> 260
<211> 486
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 34829; gene = ERU157; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179782

<400> 260
cgtggccatc tgccagccac cccaatacag cacagctatg agtccccagc tctgtgcact 60
catgctggcc atgtgctggc tgctaaccag ctgtcctgcg ttgatgcaca cgctgttgct 120
gaccctgtgtg gctttctgtg ccagaaggc catccccac ttctactgtg atccagtg 180
tctcctgaag ctgcctgct cggatacccg cataaatgag ctgatgatca tcgcatggg 240
cttgacgttc ctactattc ccctcacact gatcgtcttc tcctacgtcc gcatctcctg 300
ggctgtgctt ggcatctcgt ctcttgccg gcatgcaag gccttctcca cctgtgggtc 360
tcatctcacg gtggttctgc tcttctatgg gtctcttatg ggtgtgtatt tgcttctcc 420
gtcatcttac tctacagaga gggaaagcag gctgccattc tctacatggt gatcattccc 480
atgtta 486

<210> 261
<211> 484
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 34829; gene = ERU159; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179783

<400> 261
tgtggccatc tgcaaccac tgaggatatc catcatcatg aacagggtgt tataagtga 60
aatggctgca tgggtcttga tcataggcta tctgatctcc ttagtgcaa cagtcttgac 120
aatgatattg cctttctgtg gcaataatgt cattgatcat attacctgtg agatcctggc 180
tcttaaactc atatgctcag atatttccat gaatgtgctt atcatggcag tggcaagtat 240
tggttatatt gtgattcttc tgctgttcat ttttatctcc tatgtattca tctctcttc 300
catcctgaga attaattctt ctgaggggag aaagaaagcc ttgcaacct gttcagccca 360

```

cctgactgtg gtcattttat tctatgggtc agctcttttt atgtacatga agcctaagtc      420
aaagtacaca aaagtatctg atgaaatcat tgcactgtct tacggagtag taaccccaat      480
gttg                                              484

<210> 262
<211> 487
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU160; Accession DDBJ/EMBL/GenBank = AF179784

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 262
t gtt gcc ata tgt cac cct ctc cac tac acc acc atc atg agg gaa gag      49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Met Arg Glu Glu
    1             5             10             15

ctc tgc acc tta ttg gtg gct ata tcc tgg ctc ctg tct tgt gcc agc      97
Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
      20             25             30

tcc ctc tcc cac acc ctt ctc ctg acc cgg ctg tcc ttc tgt gct gct      145
Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
      35             40             45

aat gtc att ccc aac ttc ttc tgt gac ctt gct gct ctg ctc aag ctg      193
Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
      50             55             60

tcc tgc tca gac atc ttc ctc aat gag ctg gtc atg ttt aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
      65             70             75             80

gtg gtg gtc att acc ttg cca ttc tta tgt atc ctg gta tct tac ggc      289
Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
      85             90             95

tac att ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc tgc      337
Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
      100            105            110

aaa gca tta tcc acg tgt ggg tcc cat ctc tct gtg gtg tct ctg tac      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
      115            120            125

tac ggg gca ata ttt ggg cag tac ctt ttc cca gca tta agc aat tcc      433
Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
      130            135            140

att gac aag gac atc att gtg gct atg atg tac acg gtg gtc aca ccc      481
Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
      145            150            155            160

atg ttg                                              487
Met Leu

```

<210> 263
 <211> 162
 <212> PRT
 <213> Eulemur rubriventer

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 34829; gene = ERU160; Accession DDBJ/EMBL/GenBank = AF179784

 <400> 263

Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Ile Met Arg Glu Glu
 1 5 10 15

Leu Cys Thr Leu Leu Val Ala Ile Ser Trp Leu Leu Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Arg Leu Ser Phe Cys Ala Ala
 35 40 45

Asn Val Ile Pro Asn Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Ile Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ala Ile Phe Gly Gln Tyr Leu Phe Pro Ala Leu Ser Asn Ser
 130 135 140

Ile Asp Lys Asp Ile Ile Val Ala Met Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 264
 <211> 475
 <212> DNA
 <213> Eulemur rubriventer

<220>
 <221> misc_feature
 <222> (1)..(475)

<223> Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785

<220>

<221> CDS

<222> (2)..(475)

<223> Product = olfactory receptor

<400> 264

```
c gtg gca atc tgc aag cct ctt cat tac atg aat att atg agt cgt caa      49
  Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
    1             5             10             15

ctg tgt cac ctt ctg gtg gct ggt tcc tgg ctg gga ggc ttt ctt cac      97
Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
      20             25             30

tct att att cag att ttt atc acc atc caa tgc ccc ttt tgt ggt ccc      145
Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
      35             40             45

aac gtg att gac cac tac ttc tgt gac ctc ctg cca tta ttc aag ctt      193
Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
      50             55             60

gcc tgc acc gac acc ttt gta gag ggg ctg act gtg ttg gcc aat agt      241
Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
      65             70             75

ggc tta att ccc gtg tgc tcc ctg ttt atc ctg gtg tcc tcc tat atc      289
Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
      85             90             95

att att ctg gtg cac ttg agg aaa cat tct gca gag ggg agg cac aaa      337
Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
      100            105            110

gcc ctc tct acc tgt gcc tct cac atc acg gtg gtc att ttg ttt ttt      385
Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
      115            120            125

gga cct gcc atc ttc ctc tac atg cga cct tcc tct acc ttc aca gaa      433
Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
      130            135            140

gac aaa ctc atg ggt gtg ttg tac aca gtc atc acc ccc agt      475
Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
      145            150            155
```

<210> 265

<211> 158

<212> PRT

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(475)

<223> Taxon = 34829; gene = ERU161; Accession DDBJ/EMBL/GenBank = AF179785

<400> 265

```
Val Ala Ile Cys Lys Pro Leu His Tyr Met Asn Ile Met Ser Arg Gln
 1             5             10             15
```

```
Leu Cys His Leu Leu Val Ala Gly Ser Trp Leu Gly Gly Phe Leu His
```

094455 080901

```

                20                25                30

Ser Ile Ile Gln Ile Phe Ile Thr Ile Gln Ser Pro Phe Cys Gly Pro
   35                40                45

Asn Val Ile Asp His Tyr Phe Cys Asp Leu Leu Pro Leu Phe Lys Leu
   50                55                60

Ala Cys Thr Asp Thr Phe Val Glu Gly Leu Thr Val Leu Ala Asn Ser
   65                70                75                80

Gly Leu Ile Pro Val Cys Ser Leu Phe Ile Leu Val Ser Ser Tyr Ile
                85                90                95

Ile Ile Leu Val His Leu Arg Lys His Ser Ala Glu Gly Arg His Lys
   100                105                110

Ala Leu Ser Thr Cys Ala Ser His Ile Thr Val Val Ile Leu Phe Phe
   115                120                125

Gly Pro Ala Ile Phe Leu Tyr Met Arg Pro Ser Ser Thr Phe Thr Glu
   130                135                140

Asp Lys Leu Met Gly Val Leu Tyr Thr Val Ile Thr Pro Ser
   145                150                155

<210> 266
<211> 487
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 266
t  gtg gcc atc tcc aac ccc ccg ctc tat gtt cag gcc atg cca agg aaa      49
   Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
   1                5                10                15

ctg tgc atc tgt ttc att atc tgt tca tac act gga ggc ttt gtt aat      97
Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn
   20                25                30

gca ata ata tta acc agc aac aca ttc acg ttg gat ttt tgt ggt gac      145
Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
   35                40                45

aat gtc atc gac gac ttt ttc tgt gat gtc cca ccc ctg gtg aag ttg      193
Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
   50                55                60

```

```

gcc tgt gat gtg gaa ggg agc tac cag gct gtg ctg tac ttc ctc ctg      241
Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu
65              70              75              80

gcc tcc aac gtc atc tcc ccg gcc atg ctc atc ctc gcc tcc tac gtc      289
Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val
85              90              95

ttc atc atc gca gca gtc ttg agg gtc cgc tcc agc cgg ggc cgc ctc      337
Phe Ile Ile Ala Ala Val Leu Arg Val Arg Ser Ser Arg Gly Arg Leu
100             105             110

aag gcc ttc tcc acg tgc tcc tcc cac ctg atc tct gtt acc tta tac      385
Lys Ala Phe Ser Thr Cys Ser Ser His Leu Ile Ser Val Thr Leu Tyr
115             120             125

tac ggc tcc att ctc tac atc tac tct cgc cca agt tcc agc tat tcc      433
Tyr Gly Ser Ile Leu Tyr Ile Tyr Ser Arg Pro Ser Ser Ser Tyr Ser
130             135             140

ctc gag agg gac aaa atg gtc tct acc ttt tac acc gtg ctg ttc ccc      481
Leu Glu Arg Asp Lys Met Val Ser Thr Phe Tyr Thr Val Leu Phe Pro
145             150             155             160

acg ctc      487
Thr Leu

<210> 267
<211> 162
<212> PRT
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU162; Accession DDBJ/EMBL/GenBank = AF179786

<400> 267

Val Ala Ile Ser Asn Pro Pro Leu Tyr Val Gln Ala Met Pro Arg Lys
1              5              10              15

Leu Cys Ile Cys Phe Ile Ile Cys Ser Tyr Thr Gly Gly Phe Val Asn
20             25             30

Ala Ile Ile Leu Thr Ser Asn Thr Phe Thr Leu Asp Phe Cys Gly Asp
35             40             45

Asn Val Ile Asp Asp Phe Phe Cys Asp Val Pro Pro Leu Val Lys Leu
50             55             60

Ala Cys Asp Val Glu Gly Ser Tyr Gln Ala Val Leu Tyr Phe Leu Leu
65             70             75             80

Ala Ser Asn Val Ile Ser Pro Ala Met Leu Ile Leu Ala Ser Tyr Val
85             90             95

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115          120          125
gtg cca tgt gta ttc atc tac ttg agg cct ttc tgc agc ttc tct gtg      433
Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
130          135          140

gat aag ata ttc tct gtg ttt tac atg gtg atc aca cct atg ttg      478
Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu
145          150          155

<210> 269
<211> 159
<212> PRT
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(478)
<223> Taxon = 34829; gene = ERU163; Accession DDBJ/EMBL/GenBank = AF179787

<400> 269

Val Ala Val Cys Asn Pro Leu His Tyr Leu Thr Val Met Asn Arg Gln
1          5          10          15

Leu Cys Leu Gln Leu Val Phe Ala Cys Trp Cys Gly Gly Phe Ile His
20          25          30

Ser Val Thr Gln Val Ile Leu Val Ile Gln Leu Pro Phe Cys Gly Pro
35          40          45

Asn Lys Leu Asp Ser Phe Tyr Cys Asp Val Pro Glu Val Ile Lys Leu
50          55          60

Ala Cys Leu Asp Thr Tyr Val Val Glu Val Leu Met Val Thr Asn Ser
65          70          75          80

Gly Leu Leu Ser Leu Val Cys Phe Leu Val Leu Ile Phe Ser Tyr Ala
85          90          95

Thr Ile Leu Thr Thr Leu Arg Thr Arg Leu His Gln Gly Gln Ser Lys
100         105         110

Ala Phe Ser Thr Cys Ala Ser His Leu Met Val Val Ser Leu Ile Phe
115         120         125

Val Pro Cys Val Phe Ile Tyr Leu Arg Pro Phe Cys Ser Phe Ser Val
130         135         140

Asp Lys Ile Phe Ser Val Phe Tyr Met Val Ile Thr Pro Met Leu
145         150         155

<210> 270
<211> 487
<212> DNA

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<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 270
t  gtg gcc atc tgc aaa cct ctt cat tac aca acc atc att agc acc agg      49
   Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
   1              5              10              15

g  tt tgt atc ctt ctt gtc tgt agc tcc tgg ctt gca gga ttc ttg atc      97
   Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
              20              25              30

a  tc ttt cca cca ata atc ctt ctt ctg cag ttg gac ttc tgt gcc tcc      145
   Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
              35              40              45

a  at ata att gat cat ttt atc tgt gat tct tct cca att ctg cag ctt      193
   Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
   50              55              60

t  ct tgt aca aac act cac ttt cta gaa ctc atg gca ttt tgt tta gcc      241
   Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
   65              70              75              80

g  tg gtg aca ctc atg gtc acc ttg acc tta gtt att ctc tcc tat aca      289
   Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
              85              90              95

a  at att atc cgg aca att cta aga att cct tct atg agt caa agg aaa      337
   Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
              100              105              110

a  aa gcc ttt tcc act tgt tcc tcc cat ata ata gtt gtt tcc ctc tct      385
   Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
              115              120              125

t  at ggt agt tgt atc ttc atg tac ata aag cct tct aca agg gaa agg      433
   Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
              130              135              140

g  tg act tta agc aaa gga gta gct gtg gtt aat act tca gtg gct cct      481
   Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
   145              150              155              160

c  tt ttg
   Leu Leu
                                         487

<210> 271
<211> 162
<212> PRT
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(487)

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<223> Taxon = 34829; gene = ERU164; Accession DDBJ/EMBL/GenBank = AF179788

<400> 271

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Ile Ser Thr Arg
1 5 10 15

Val Cys Ile Leu Leu Val Cys Ser Ser Trp Leu Ala Gly Phe Leu Ile
20 25 30

Ile Phe Pro Pro Ile Ile Leu Leu Leu Gln Leu Asp Phe Cys Ala Ser
35 40 45

Asn Ile Ile Asp His Phe Ile Cys Asp Ser Ser Pro Ile Leu Gln Leu
50 55 60

Ser Cys Thr Asn Thr His Phe Leu Glu Leu Met Ala Phe Cys Leu Ala
65 70 75 80

Val Val Thr Leu Met Val Thr Leu Thr Leu Val Ile Leu Ser Tyr Thr
85 90 95

Asn Ile Ile Arg Thr Ile Leu Arg Ile Pro Ser Met Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Ile Lys Pro Ser Thr Arg Glu Arg
130 135 140

Val Thr Leu Ser Lys Gly Val Ala Val Val Asn Thr Ser Val Ala Pro
145 150 155 160

Leu Leu

<210> 272

<211> 483

<212> DNA

<213> Eulemur rubriventer

<220>

<221> misc_feature

<222> (1)..(483)

<223> Taxon = 34829; gene = ERU165; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179789

<400> 272

cgttgccatc tgcaagcccc tccactaccc ccgtgctcat gagcagcagg gtctgcacac 60

agctcatcct cgctgctgg ctggcagggt tctccttcat cattgtgcct gtcacacctga 120

ccagtcagct tccattctgt gacacccaca tcaaccactt cttctgtgac tatacacctc 180

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taatggaggt ggtctgcagt gggccaaagg tgctggagat ggtggatttt accctggcct 240
tggtggcact gctcagcacc ttgggtgctga tcaccctgtc ctacatccag atcatcagga 300
cgattgtcag gatccccctct gtccaggaga ggaaaaaggc tttctccacc tggtcctccc 360
atgtcatcgt ggttaccatg tgctatggaa gctgtttttt tatgtatgtc aagccctccc 420
caggcaaagg ggttgatcta aacaaaggag tgtcttaatc aatacaatta ttgccccctt 480
ctt 483

<210> 273
<211> 486
<212> DNA
<213> Eulemur rubriventer

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 34829; gene = ERU167; Accession DDBJ/EMBL/GenBank = AF179790

<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor

<400> 273
t gtg gcc atc tgt cac cct ctg aga tac aca gac atc atg act cct cgt 49
  Val Ala Ile Cys His Pro Leu Arg Tyr Thr Asp Ile Met Thr Pro Arg
  1 5 10 15

ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat 97
Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
  20 25 30

gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac 145
Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
  35 40 45

ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc 193
Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
  50 55 60

gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct 241
Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
  65 70 75 80

tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act 289
Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
  85 90 95

caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat 337
Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
  100 105 110

aaa gcc ttt tcc acc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc 385
Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
  115 120 125

tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct 433
Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
  130 135 140

tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc 481

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<212> DNA
 <213> Eulemur rubriventer
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 34829; gene = ERU168; Accession DDBJ/EMBL/GenBank = AF179791

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 275
 t gtg gcc atc tgt cac cct ctg aca tac aca gac atc atg act cct cgt 49
 Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg
 1 5 10 15
 ctg tgt ggt ctg ctg gtt tca ctt tcc ctg tcc att tgc tcc gcg gat 97
 Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
 20 25 30
 gcc ctg ctc cac agc ctc atg ctg ctg cag ctg tcc ttc tgc aca gac 145
 Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
 35 40 45
 ctt gaa atc tcc ctt ttc ttc tgt gaa gtc gtt cag gtc gtc aag ctc 193
 Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
 50 55 60
 gcg tgc tcc gat acc ctc gtc aac aac ctt ctg atc tat ttt gca gct 241
 Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
 65 70 75 80
 tgc acc ttg ggt ggc att cct ctg tct ggc atc att ttt tct tac act 289
 Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
 85 90 95
 caa ata gcc acc tcc att ttg aaa atg ccg tca tcg ggc aga aag tat 337
 Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
 100 105 110
 aaa gcc ttt tcc gcc tgt ggg tct cac ctg tca gtt gtt tcc ctg ttc 385
 Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125
 tat ggg aca ggt ttg ggg gtg tac atc agt tct gca gtt tct gac tct 433
 Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
 130 135 140
 tca agg agg act gcg gtg gct tca gtg atg tac act gtg gtc act ccc 481
 Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160
 gtg ttg 487
 Val Leu

<210> 276
 <211> 162
 <212> PRT
 <213> Eulemur rubriventer

<220>
 <221> misc_feature

<222> (1)..(487)
 <223> Taxon = 34829; gene = ERU168; Accession DDBJ/EMBL/GenBank = AF179791
 <400> 276

Val Ala Ile Cys His Pro Leu Thr Tyr Thr Asp Ile Met Thr Pro Arg
 1 5 10 15

Leu Cys Gly Leu Leu Val Ser Leu Ser Leu Ser Ile Cys Ser Ala Asp
 20 25 30

Ala Leu Leu His Ser Leu Met Leu Leu Gln Leu Ser Phe Cys Thr Asp
 35 40 45

Leu Glu Ile Ser Leu Phe Phe Cys Glu Val Val Gln Val Val Lys Leu
 50 55 60

Ala Cys Ser Asp Thr Leu Val Asn Asn Leu Leu Ile Tyr Phe Ala Ala
 65 70 75 80

Cys Thr Leu Gly Gly Ile Pro Leu Ser Gly Ile Ile Phe Ser Tyr Thr
 85 90 95

Gln Ile Ala Thr Ser Ile Leu Lys Met Pro Ser Ser Gly Arg Lys Tyr
 100 105 110

Lys Ala Phe Ser Ala Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125

Tyr Gly Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Ser Asp Ser
 130 135 140

Ser Arg Arg Thr Ala Val Ala Ser Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Val Leu

<210> 277
 <211> 486
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792

<220>
 <221> CDS
 <222> (1)..(486)
 <223> Product = olfactory receptor

<400> 277
 cct gcc atc tgc cag cca ctc agg tac cgc gtg ctc atg aac cac cgg

48

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Pro Ala Ile Cys Gln Pro Leu Arg Tyr Arg Val Leu Met Asn His Arg
1          5          10          15

ctc tgt gtg ctg ctg gtg gga gct gcc tgg gtc ctc tgc ctc ctc aag      96
Leu Cys Val Leu Leu Val Gly Ala Ala Trp Val Leu Cys Leu Leu Lys
          20          25          30

tcg gtg act gag aca gtc att gcc atg agg ctg ccc ttc tgt ggc cac      144
Ser Val Thr Glu Thr Val Ile Ala Met Arg Leu Pro Phe Cys Gly His
          35          40          45

cac gtg gtc agt cac ttc acc tgc gag atc ctg gcg gtg ctg aag ctg      192
His Val Val Ser His Phe Thr Cys Glu Ile Leu Ala Val Leu Lys Leu
          50          55          60

acg tgc ggt aac aca tcg gtc agc gag gtc ttc ctg ctg gtg ggc tcc      240
Thr Cys Gly Asn Thr Ser Val Ser Glu Val Phe Leu Leu Val Gly Ser
          65          70          75          80

atc ctg ctg ctg cct gtg ccc ctg gca ttc att tgc ctg tcc tac ttg      288
Ile Leu Leu Leu Pro Val Pro Leu Ala Phe Ile Cys Leu Ser Tyr Leu
          85          90          95

ctc atc ctg gcc acc atc ctg agg gtg ccc tca gct gct ggg tgc cgc      336
Leu Ile Leu Ala Thr Ile Leu Arg Val Pro Ser Ala Ala Gly Cys Arg
          100          105          110

aaa gcc ttc tcc acc tgc tca gca cac ctg gct gtg gtg ctg ctt ttc      384
Lys Ala Phe Ser Thr Cys Ser Ala His Leu Ala Val Val Leu Leu Phe
          115          120          125

tac agc acc atc atc ttc acg tac atg aag ccc aag agc aag gaa gcc      432
Tyr Ser Thr Ile Ile Phe Thr Tyr Met Lys Pro Lys Ser Lys Glu Ala
          130          135          140

cac atc tct gat gag gtc ttc aca gtc ctc tac gcc atg gtc aca ccc      480
His Ile Ser Asp Glu Val Phe Thr Val Leu Tyr Ala Met Val Thr Pro
          145          150          155          160

atg ttg
Met Leu
          486

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<210> 278
<211> 162
<212> PRT
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9546; gene = MSY172; Accession DDBJ/EMBL/GenBank = AF179792

<400> 278

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Pro Ala Ile Cys Gln Pro Leu Arg Tyr Arg Val Leu Met Asn His Arg
1          5          10          15

Leu Cys Val Leu Leu Val Gly Ala Ala Trp Val Leu Cys Leu Leu Lys
          20          25          30

Ser Val Thr Glu Thr Val Ile Ala Met Arg Leu Pro Phe Cys Gly His
          35          40          45

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<211> 481
 <212> DNA
 <213> Macaca sylvanus

 <220>
 <221> misc_feature
 <222> (1)..(4818)
 <223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794

 <220>
 <221> CDS
 <222> (2)..(481)
 <223> product = olfactory receptor

<400> 280
 t gtg gcc atc tgt aag ccc ttg cac tat gca acc atc atg agt caa cct 49
 Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
 1 5 10 15

 atg tgt gga ttc ctg atg ggg gtg gct ggg att ctg gga ttt gtg cat 97
 Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
 20 25 30

 gga ggg atc cag act ttg ttc ata gcc cac tta cca ttc tgt ggc cct 145
 Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
 35 40 45

 aat gtc atc gac cac ttt atg tgt gat tta gta cct ctt cta gag ctg 193
 Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
 50 55 60

 gcc tgc aca gac act cac acc ttg ggg cct ctg ata gct gcc aac agt 241
 Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
 65 70 75 80

 gga tca ttg tgt ttc ctc att ttt tcc atg ctg gtt gct tcc tat gtc 289
 Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
 85 90 95

 atc atc ctg tgc tcc cta agg act cat atc tct gaa ggg cgt cac aaa 337
 Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
 100 105 110

 gtt ctg tct agt tgt acc tct cat atc ttt gtt gtc atc tta ttc ttt 385
 Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
 115 120 125

 gtc cct tgt tca tac ctg tat cta aga cct cta acc tcc ttc ttc ccc 433
 Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
 130 135 140

 act gac aaa gct gtg act gtg ttt tgc acc cta ttt aca cct atg ttg 481
 Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
 145 150 155 160

<210> 281
 <211> 160
 <212> PRT
 <213> Macaca sylvanus

 <220>
 <221> misc_feature
 <222> (1)..(4818)
 <223> Taxon = 9546; gene = MSY174; Accession DDBJ/EMBL/GenBank = AF179794

<400> 281

Val Ala Ile Cys Lys Pro Leu His Tyr Ala Thr Ile Met Ser Gln Pro
1 5 10 15

Met Cys Gly Phe Leu Met Gly Val Ala Gly Ile Leu Gly Phe Val His
20 25 30

Gly Gly Ile Gln Thr Leu Phe Ile Ala His Leu Pro Phe Cys Gly Pro
35 40 45

Asn Val Ile Asp His Phe Met Cys Asp Leu Val Pro Leu Leu Glu Leu
50 55 60

Ala Cys Thr Asp Thr His Thr Leu Gly Pro Leu Ile Ala Ala Asn Ser
65 70 75 80

Gly Ser Leu Cys Phe Leu Ile Phe Ser Met Leu Val Ala Ser Tyr Val
85 90 95

Ile Ile Leu Cys Ser Leu Arg Thr His Ile Ser Glu Gly Arg His Lys
100 105 110

Val Leu Ser Ser Cys Thr Ser His Ile Phe Val Val Ile Leu Phe Phe
115 120 125

Val Pro Cys Ser Tyr Leu Tyr Leu Arg Pro Leu Thr Ser Phe Phe Pro
130 135 140

Thr Asp Lys Ala Val Thr Val Phe Cys Thr Leu Phe Thr Pro Met Leu
145 150 155 160

<210> 282

<211> 402

<212> DNA

<213> *Macaca sylvanus*

<220>

<221> misc_feature

<222> (1)..(402)

<223> Taxon = 9546; gene = MSY175; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179795*

<400> 282

tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcatgca 60

gcttgtgctt ggggtgttggc ttgctgggtt ctcgtcacct ttccaccact cctcttaggc 120

ctaaatcttg acttctgtgc ctgcctccaa cgtcattaat catttctact gtgacactac 180

tccactcctg cagatttcct gcactgacac acagctcctg gacaggatgg gattcatttc 240

agcattgggtg acactcttag tcacattggg aatgggtgatg gtatcatgat atccctttct 300

tatggcagtt gcattctcat gtatgttaag ccatcgggtca aacaaaagat atatttttca 360

aagggaattt tgggtgctcaa cacctctgtc gtccacttt tg

402

<210> 283
<211> 487
<212> DNA
<213> *Macaca sylvanus*

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 283
c gtg gct att tgc aac cct ctg ctc tac gca tta gtg gtg tct cca aag 49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
1 5 10 15

gta tgt cgt ctg ctg gtg tcc ctc aca tac ctt cag agt ctt atc aca 97
Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
20 25 30

gcc ctt act gtc tct tcc tgt gtg ttc tct gtg tca tac tgt tct tcc 145
Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
35 40 45

aac atc atc aac cat ttt tac tgt gac gat gtc cct ttg cta gca ttg 193
Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
50 55 60

tcg tgt tct gat acc tac att cca gaa aca gca gtg ttt atc ttt tca 241
Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
65 70 75 80

ggg acc aat ttg ttt ttc tcc atg acc gtt gtt ctg ata tcc tac ttc 289
Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
85 90 95

aac att gtt att acc att ttg agg ata cgt tcc tca gaa gga cga caa 337
Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
100 105 110

aaa gcc ttt tcc acg tgt gct tct cac atg ata gct gtg gtt gtg ttc 385
Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val Phe
115 120 125

tat ggg act ctc ctt ttc atg tat ttg caa cca agg agt aat cac tca 433
Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
130 135 140

tta gat act gac aaa atg gcc tcg gtc ttc tac acc ctg atc ata cct 481
Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
145 150 155 160

atg ttg 487
Met Leu

<210> 284

<211> 162
 <212> PRT
 <213> *Macaca sylvanus*

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY176; Accession DDBJ/EMBL/GenBank = AF179796

 <400> 284

Val Ala Ile Cys Asn Pro Leu Leu Tyr Ala Leu Val Val Ser Pro Lys
 1 5 10 15

Val Cys Arg Leu Leu Val Ser Leu Thr Tyr Leu Gln Ser Leu Ile Thr
 20 25 30

Ala Leu Thr Val Ser Ser Cys Val Phe Ser Val Ser Tyr Cys Ser Ser
 35 40 45

Asn Ile Ile Asn His Phe Tyr Cys Asp Asp Val Pro Leu Leu Ala Leu
 50 55 60

Ser Cys Ser Asp Thr Tyr Ile Pro Glu Thr Ala Val Phe Ile Phe Ser
 65 70 75 80

Gly Thr Asn Leu Phe Phe Ser Met Thr Val Val Leu Ile Ser Tyr Phe
 85 90 95

Asn Ile Val Ile Thr Ile Leu Arg Ile Arg Ser Ser Glu Gly Arg Gln
 100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Met Ile Ala Val Val Val Phe
 115 120 125

Tyr Gly Thr Leu Leu Phe Met Tyr Leu Gln Pro Arg Ser Asn His Ser
 130 135 140

Leu Asp Thr Asp Lys Met Ala Ser Val Phe Tyr Thr Leu Ile Ile Pro
 145 150 155 160

Met Leu

<210> 285
 <211> 487
 <212> DNA
 <213> *Macaca sylvanus*

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797

 <220>

<221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

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<400> 285
t gtg gcc atc tgt cac cct cta cat tat gcc atc atc atg ggt cag agt      49
  Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
    1             5             10             15

cag tgt gtc acg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt      97
Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
          20             25             30

gct ctt ttg cac act ctc ctc ctg gcc tgg ctt tcc ttc tgt gct gat      145
Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
          35             40             45

cac atc atc cct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ttg      193
His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
          50             55             60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga      241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
          65             70             75             80

ttg aca gcc att atg ctt cca ttc ctg tgt atc ctg gtt tct tat ggt      289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
          85             90             95

cac act gca gtc acc atc ctc cag att ccc tct act aat ggc ata tgc      337
His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
          100            105            110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gca gtg act ctc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
          115            120            125

tat ggg acc att att ggt ctc tat ttt ctt ccc cca tcc agc aac act      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
          130            135            140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc      481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
          145            150            155            160

atg ttg      487
Met Leu
  
```

```

<210> 286
<211> 162
<212> PRT
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY177; Accession DDBJ/EMBL/GenBank = AF179797

<400> 286
  
```

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Val Ala Ile Cys His Pro Leu His Tyr Ala Ile Ile Met Gly Gln Ser
1             5             10             15
  
```

Gln Cys Val Thr Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30

Ala Leu Leu His Thr Leu Leu Leu Ala Trp Leu Ser Phe Cys Ala Asp
 35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
 65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
 85 90 95

His Thr Ala Val Thr Ile Leu Gln Ile Pro Ser Thr Asn Gly Ile Cys
 100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Ala Val Thr Leu Tyr
 115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
 130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 287
 <211> 487
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY178; Accession DDBJ/EMBL/GenBank = AF179798

<220>
 <221> CDS
 <222> (2)..(487)
 <223> product = olfactory receptor

<400> 287
 t gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg 49
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
 1 5 10 15

ctc tgt ctc gcc ctg gtg gcg ctg tcc tgg gta ctg acc acc ttc cat 97
 Leu Cys Leu Ala Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac 145
 Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp

Leu Ile Val Arg Ala Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr
 100 105 110
 aaa gcc ttc tcc act tgt gcc tcc cat ttg ggt gta gtc tcc ctc ttc 385
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Gly Val Val Ser Leu Phe
 115 120 125
 tat ggg aca ctt tgt atg gta tac ctg aag ccc ctc cat acc tac tct 433
 Tyr Gly Thr Leu Cys Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser
 130 135 140
 gtg aag gac tca gta gcc aca gtg atg tat gcg gtg gtg aca ccc atg 481
 Val Lys Asp Ser Val Ala Thr Val Met Tyr Ala Val Val Thr Pro Met
 145 150 155 160
 atg 484
 Met

<210> 290
 <211> 161
 <212> PRT
 <213> Macaca sylvanus
 <220>
 <221> misc_feature
 <222> (1)..(484)
 <223> Taxon = 9546; gene = MSY179; Accession DDBJ/EMBL/GenBank = AF179799
 <400> 290

Cys Ala Ile Cys Cys Pro Leu His Tyr Thr Thr Ala Met Ser Pro Lys
 1 5 10 15
 Leu Cys Ile Leu Leu Leu Ser Leu Cys Trp Val Leu Ser Val Leu Tyr
 20 25 30
 Gly Leu Ile His Thr Phe Leu Met Thr Thr Val Thr Phe Cys Gly Ser
 35 40 45
 Arg Lys Ile His Tyr Ile Phe Cys Glu Met Tyr Val Leu Leu Arg Leu
 50 55 60
 Ala Cys Ser Asp Thr Gln Ile Asn His Thr Val Leu Ile Ala Thr Gly
 65 70 75 80
 Cys Phe Ile Phe Leu Ile Pro Phe Gly Phe Met Ile Ile Ser Tyr Val
 85 90 95
 Leu Ile Val Arg Ala Ile Leu Arg Ile Pro Ser Val Ser Lys Lys Tyr
 100 105 110
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Gly Val Val Ser Leu Phe
 115 120 125
 Tyr Gly Thr Leu Cys Met Val Tyr Leu Lys Pro Leu His Thr Tyr Ser
 130 135 140

Val Lys Asp Ser Val Ala Thr Val Val Met Tyr Ala Val Val Thr Pro Met
 145 150 155 160

Met

<210> 291
 <211> 487
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY180; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179800

<400> 291
 tgctgccata tgtcaccctc tccattacac tgccatcatg agggaagagc tctgtgtctt 60
 cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cctttctcct 120
 gaccagctg tctttctgtg ctgcgaacac catccccac atcttctgtg accttgctgc 180
 cctgctcaag ctgtcctggt cagatatctt cctcaatgag ctggatcatgt tcacagtagg 240
 ggtggtgggc attaccctgc cattcatgtg tatcctggta tcatatggct aactgggggc 300
 caccatcctg aggggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc 360
 ccatctctct gtgggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac 420
 tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc 480
 cgtgttg 487

<210> 292
 <211> 487
 <212> DNA
 <213> Macaca sylvanus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY181; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179801

<400> 292
 tgctgccata tgtcaccctc tccattacac tgccatcatg agggaagagc tctgtgtctt 60
 cttagtggct gtatcttgaa ttctgtcttg tgccagctcc ctctctcaca cctttctcct 120
 gaccagctg tctttctgtg ctgcgaacac catccccac atcttctgtg accttgctgc 180
 cctgctcaag ctgtcctggt cagatatctc cctcaatgag ctggatcatgt tcacagtagg 240
 ggtggtgggc attaccctgc cattcatgtg tatcctggta tcatatggct aactgggggc 300
 caccatcctg aggggtccctt caaccaaagg gatccacaaa gcattgtcca catgtgcctc 360
 ccatctctct gtgggtttctc tctattatgg gtcaatattt ggccagtaac atttcccaac 420

```

tgtaagcagt tctattgaca aggatgttac tgtggctctc atgtacatcg tggtcacacc      480
cgtgttg                                                                    487

<210> 293
<211> 487
<212> DNA
<213> Macaca sylvanus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 293
t  gtg gcc atc tgt aaa ccc ctt cat tat atg gtc atc atg aac aac agg      49
   Val Ala Ile Cys Lys Pro Leu His Tyr Met Val Ile Met Asn Asn Arg
   1              5              10              15

gtg tgt acc tta tta gtc ctc tgc agt tgg gtg gct ggc ttg atg atc      97
Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
      20              25              30

att gtt cca cca ctg agc tta ggc ctc cag ctc gaa ttc tgt ggc tcc      145
Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
      35              40              45

aat gcc att gat cat ttt agc tgt gat gca ggt cct ctc cta aag atc      193
Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
      50              55              60

tca tgc tca gac aca tgg gta ata gaa cag ata gtt ata ctt atg gct      241
Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
      65              70              75

gta ttt gca ctc att atc acc cta gtt tgt gtg att ctg tcc tac ttg      289
Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
      85              90              95

tac ata gtc aga aca att ctg agg ttc cct tct gtt cag caa agg aaa      337
Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
      100             105             110

aag gcc ttt tct acc tgt tca tcc cac atg att gtg gtt tcc att gcc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
      115             120             125

tat gga agc tgc atc ttc gtc tat atc aag ccc tct gca aaa gat gaa      433
Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
      130             135             140

gtg gcc ata aat aaa gga gtt tca gtt ctt act act tct gtt gca ccc      481
Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
      145             150             155

ttg ttg                                                                    487
Leu Leu

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<210> 294
 <211> 162
 <212> PRT
 <213> *Macaca sylvanus*

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9546; gene = MSY182; Accession DDBJ/EMBL/GenBank = AF179802

 <400> 294

Val Ala Ile Cys Lys Pro Leu His Tyr Met Val Ile Met Asn Asn Arg
 1 5 10 15

Val Cys Thr Leu Leu Val Leu Cys Ser Trp Val Ala Gly Leu Met Ile
 20 25 30

Ile Val Pro Pro Leu Ser Leu Gly Leu Gln Leu Glu Phe Cys Gly Ser
 35 40 45

Asn Ala Ile Asp His Phe Ser Cys Asp Ala Gly Pro Leu Leu Lys Ile
 50 55 60

Ser Cys Ser Asp Thr Trp Val Ile Glu Gln Ile Val Ile Leu Met Ala
 65 70 75 80

Val Phe Ala Leu Ile Ile Thr Leu Val Cys Val Ile Leu Ser Tyr Leu
 85 90 95

Tyr Ile Val Arg Thr Ile Leu Arg Phe Pro Ser Val Gln Gln Arg Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Val Ser Ile Ala
 115 120 125

Tyr Gly Ser Cys Ile Phe Val Tyr Ile Lys Pro Ser Ala Lys Asp Glu
 130 135 140

Val Ala Ile Asn Lys Gly Val Ser Val Leu Thr Thr Ser Val Ala Pro
 145 150 155 160

Leu Leu

<210> 295
 <211> 487
 <212> DNA
 <213> *Callithrix jacchus*

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 295
 t gtg gcc att tgc cgc ccc ctg tac tac tcc aca gtc atg agc ccc caa 49
 Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
 1 5 10 15
 gtc tgt gcc cta atc ctt gca ttg tgc tgg gtc ctc acc aat gtt gtt 97
 Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
 20 25 30
 gcc ctg act cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act 145
 Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45
 ggg gaa ata gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta 193
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60
 tca tgt tct gac acc cac atc aac gag atg atg gtt ttt gtc ttg gga 241
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80
 ggc aca gta ctc att gtc ccc ttt ata tgc att gtc acc tcc tac atc 289
 Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
 85 90 95
 cac att gtg cct gct atc ctg agg gtc cga acc tgt ggt ggg gcg ggc 337
 His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
 100 105 110
 aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt ata ttc 385
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
 115 120 125
 tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tct att gcc tct 433
 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
 130 135 140
 gaa gag aag gac att gca gca gct gca ctg tat acc ata gtg act ccc 481
 Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
 145 150 155 160
 atg ttg 487
 Met Leu

<210> 296
 <211> 162
 <212> PRT
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA169; Accession DDBJ/EMBL/GenBank = AF179803
 <400> 296

Val Ala Ile Cys Arg Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
 1 5 10 15

Val Cys Ala Leu Ile Leu Ala Leu Cys Trp Val Leu Thr Asn Val Val
20 25 30

Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
35 40 45

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
65 70 75 80

Gly Thr Val Leu Ile Val Pro Phe Ile Cys Ile Val Thr Ser Tyr Ile
85 90 95

His Ile Val Pro Ala Ile Leu Arg Val Arg Thr Cys Gly Gly Ala Gly
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Ile Phe
115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
130 135 140

Glu Glu Lys Asp Ile Ala Ala Ala Ala Leu Tyr Thr Ile Val Thr Pro
145 150 155 160

Met Leu

<210> 297
<211> 486
<212> DNA
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/GenBank = AF179804

<220>
<221> CDS
<222> (1)..(486)
<223> Product = olfactory receptor

<400> 297
gtg gcc atc tgt cac cca ctg cac tac aca gtc acc att aac ccc aga 48
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1 5 10 15
ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 96
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20 25 30

tcc Ser	tca Ser	tta Leu	caa Gln	acc Thr	tta Leu	ata Ile	gtg Val	ctg Leu	cgg Arg	ctt Leu	tcc Ser	ttc Phe	tgc Cys	aca Thr	gac Asp	144
35						40			45							
ttg Leu	gaa Glu	atc Ile	ccc Pro	cgc Arg	ttt Phe	ttc Phe	tgc Cys	gaa Glu	ctt Leu	aat Asn	cag Gln	gtc Val	atc Ile	cac His	ctt Leu	192
50						55			60							
gcc Ala	tgt Cys	tct Ser	gac Asp	act Thr	ttt Phe	ctt Leu	aat Asn	gat Asp	gtg Val	gtg Val	atg Met	tat Tyr	ttg Leu	gcc Ala	gct Ala	240
65			70						75			80				
gtg Val	ctg Leu	ctg Leu	ggg Gly	ggg Gly	ggg Gly	ccc Pro	ctt Leu	gca Ala	ggg Gly	att Ile	ctt Leu	tac Tyr	tct Ser	tac Tyr	tct Ser	288
			85						90			95				
aag Lys	ata Ile	gtt Val	tcc Ser	tcc Ser	ata Ile	cgt Arg	gca Ala	atc Ile	tca Ser	tca Ser	gct Ala	cag Gln	ggg Gly	aag Lys	tac Tyr	336
			100			105						110				
aag Lys	gca Ala	ttt Phe	tcc Ser	acc Thr	tgt Cys	gta Val	tct Ser	cac His	atc Ile	tta Leu	att Ile	gtc Val	tcc Ser	tta Leu	ttt Phe	384
115						120						125				
tat Tyr	ggg Gly	aca Thr	ctc Leu	cta Leu	ggg Gly	gtg Val	tac Tyr	ctt Leu	agt Ser	tct Ser	gct Ala	gca Ala	act Thr	ggc Gly	aac Asn	432
130						135			140							
tca Ser	cat His	tca Ser	aga Arg	gct Ala	gca Ala	gcc Ala	tcg Ser	gtg Val	atg Met	tac Tyr	act Thr	gtg Val	gtc Val	acc Thr	ccc Pro	480
145			150						155			160				
atg Met			ctg Leu													486

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<210> 298
<211> 162
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9483; gene = CJA170; Accession DDBJ/EMBL/GenBank = AF179804

<400> 298
```

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20 25 30

Leu Glu Ile Pro Arg Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50 55 60


```

ttt att ctt tcc agc att ctc cac att agt tct gct gag ggc agg tct      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser
      100                      105                      110

aaa gcc ttc agt acc tgc agc tcc cac ata gtt gtg gta ttg ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe
      115                      120                      125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
      130                      135                      140

ctg gac cag ggg aaa gtg tcc tcc att ttt tat act gcg gtg gtg ccc      481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
      145                      150                      155                      160

atg ttt                                                                487
Met Phe

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<210> 300
<211> 162
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9483; gene = CJA171; Accession DDBJ/EMBL/GenBank = AF179805

<400> 300

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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1          5          10          15

```

```

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Ala Leu Gly
      20          25          30

```

```

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ala Glu
      35          40          45

```

```

Thr Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
      50          55          60

```

```

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
      65          70          75          80

```

```

Thr Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
      85          90          95

```

```

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Ala Glu Gly Arg Ser
      100          105          110

```

```

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Val Val Val Leu Leu Phe
      115          120          125

```

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
 145 150 155 160

Met Phe

<210> 301
 <211> 487
 <212> DNA
 <213> *Callithrix jacchus*
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA196; Accession DDBJ/EMBL/GenBank = AF179806

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 301
 c ttg gcc atc tgc cac ccg ctg cac tac tcc tcc aag atg agc ctg tgc 49
 Leu Ala Ile Cys His Pro Leu His Tyr Ser Ser Lys Met Ser Leu Cys
 1 5 10 15
 agc tgc acc cta atg ttg ggc tgc tta tgg acc act gcc agc ctc cat 97
 Ser Cys Thr Leu Met Leu Gly Cys Leu Trp Thr Thr Ala Ser Leu His
 20 25 30
 gcc ctt ctg cac acc ctt ctc ttg gcc cgg ctg gac ttc tgt gcc agc 145
 Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Asp Phe Cys Ala Ser
 35 40 45
 aat gtt atc ccc tac ttc ttc tgt gac ctc gtt ccc ctg ctc cag ctc 193
 Asn Val Ile Pro Tyr Phe Phe Cys Asp Leu Val Pro Leu Leu Gln Leu
 50 55 60
 tcc tgt tct gac acc cga ctc aac cag ctc atg att gtg ctg gtg ggg 241
 Ser Cys Ser Asp Thr Arg Leu Asn Gln Leu Met Ile Val Leu Val Gly
 65 70 75 80
 ggc ctg atc atc ctc ctg ccc ttc ctt ggc att ctc ggt tcc tac aca 289
 Gly Leu Ile Ile Leu Leu Pro Phe Leu Gly Ile Leu Gly Ser Tyr Thr
 85 90 95
 tgc att gca gct gca gtg ctc aga gtc ccc tct gcc agg ggt acg tgg 337
 Cys Ile Ala Ala Ala Val Leu Arg Val Pro Ser Ala Arg Gly Thr Trp
 100 105 110
 aag gcc ttt tcc acc tgt ggc tcc cac ctg acc atg gtc atc ctc ttc 385
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Thr Met Val Ile Leu Phe
 115 120 125
 tat ggc acc atc tca ggg gtc tac ctg agg ccc tca tcc tcc cac tcc 433
 Tyr Gly Thr Ile Ser Gly Val Tyr Leu Arg Pro Ser Ser Ser His Ser
 130 135 140
 aca gac aag gac tca cta gcc tca gtg atg tac atg gta gtg acc ccc 481
 Thr Asp Lys Asp Ser Leu Ala Ser Val Met Tyr Met Val Val Thr Pro

<223> Taxon = 9483; gene = CJA197; Accession DDBJ/EMBL/GenBank = AF179807

<400> 304

Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1 5 10 15

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20 25 30

Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50 55 60

Ala Cys Ser Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
65 70 75 80

Val Leu Leu Gly Gly Gly Pro Leu Ala Gly Ile Leu Tyr Ser Tyr Ser
85 90 95

Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Val Ser His Ile Leu Ile Val Ser Leu Phe
115 120 125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
130 135 140

Ser His Ser Arg Ala Ala Ala Ser Val Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 305

<211> 487

<212> DNA

<213> Callithrix jacchus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 305

c att gcc atc tgt agc ccc ttg ctg tac aat gtc atc atg tcc tat cac
Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His

49

```

1             5             10             15
ttc tgc ttc cgg ctc aca gtg gga gtt tac att tta ggc atc ctt gga      97
Phe Cys Phe Arg Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly
                20                25                30

tct aca att cac acc agc tct atg ttg aga ctc ttt ctg tgc aaa act      145
Ser Thr Ile His Thr Ser Ser Met Leu Arg Leu Phe Leu Cys Lys Thr
                35                40                45

aat gtg att aac cat tat ttt tgt gat ctc ttc cct ctc ttg gaa ctc      193
Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu
                50                55                60

tcc tgc tcc agt acc tac atc aat gaa tta cta gtt ctg gtc ttg agt      241
Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser
        65                70                75                80

gca ttg aat atc ctg acg cct gcc tta act atc ctg gcc tct tat atc      289
Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile
                85                90                95

ttc acc att gcc agt atc ctc cac att cgc tcc act gag ggc agg tcc      337
Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser
                100                105                110

aaa gcc ttc agc act tgc agc tcc cac atc tca gct gtt gct gtc ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe
                115                120                125

ttt gga tct gca gca ttc atg tac ctg cag cca tca tct gtc agt tcc      433
Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser
                130                135                140

atg gac cag ggg aaa gtg tca tct gtg ttt tac aca act gtt gtg ccc      481
Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro
        145                150                155                160

atg ctg
Met Leu
                487

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<210> 306
<211> 162
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9483; gene = CJA198; Accession DDBJ/EMBL/GenBank = AF179808

<400> 306

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Ile Ala Ile Cys Ser Pro Leu Leu Tyr Asn Val Ile Met Ser Tyr His
1             5             10             15

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Phe Cys Phe Arg Leu Thr Val Gly Val Tyr Ile Leu Gly Ile Leu Gly
                20                25                30

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Ser Thr Ile His Thr Ser Ser Met Leu Arg Leu Phe Leu Cys Lys Thr
                35                40                45

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Asn Val Ile Asn His Tyr Phe Cys Asp Leu Phe Pro Leu Leu Glu Leu
50 55 60

Ser Cys Ser Ser Thr Tyr Ile Asn Glu Leu Leu Val Leu Val Leu Ser
65 70 75 80

Ala Leu Asn Ile Leu Thr Pro Ala Leu Thr Ile Leu Ala Ser Tyr Ile
85 90 95

Phe Thr Ile Ala Ser Ile Leu His Ile Arg Ser Thr Glu Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ser Ala Val Ala Val Phe
115 120 125

Phe Gly Ser Ala Ala Phe Met Tyr Leu Gln Pro Ser Ser Val Ser Ser
130 135 140

Met Asp Gln Gly Lys Val Ser Ser Val Phe Tyr Thr Thr Val Val Pro
145 150 155 160

Met Leu

<210> 307
<211> 469
<212> DNA
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(469)
<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809

<220>
<221> CDS
<222> (2)..(469)
<223> Product = olfactory receptor

<400> 307
t gtt gct atc tgt cac ccc ctg cac tac acc act gtc atg agt cgg gga 49
Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly
1 5 10 15

tta tgc tgt gtg ttg gtt gct gcc tcc tgg atg gga gga ttt gtg cac 97
Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His
20 25 30

tcc acc gtc cag acc att ctc act atc cgt ctg ccc ttt tgt ggg cca 145
Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro
35 40 45

aat cag gtg gac aac ttt ttt tgt gat gtt ccc cct gtc atc aaa ctt 193
Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu
50 55 60

gcc tgt gct gac act ttt gtc att gaa ttg ctc atg gta tct aac agt 241

Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met Val Ser Asn Ser
65 70 75 80

ggg ttg atc tcc acc agc tcc ttt gtg gtg ctg att tcc tcc tac acc 289
Gly Leu Ile Ser Thr Ser Ser Phe Val Val Leu Ile Ser Ser Tyr Thr
85 90 95

act atc cta gtc aag att cac tcc aag gag gga agg cga aag gca ctc 337
Thr Ile Leu Val Lys Ile His Ser Lys Glu Gly Arg Arg Lys Ala Leu
100 105 110

tcc aca tgt gcc tct cac ctt atg gtg gta aca ctt ttt gga ccc tgt 385
Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Gly Pro Cys
115 120 125

agt ttc atc tat cct cat cct ttc tct aca ttt tct gtg gac aag atg 433
Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met
130 135 140

gtg tct gta ctc tac aag gtt att act cca atg cta 469
Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu
145 150 155

<210> 308
<211> 156
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(469)
<223> Taxon = 9483; gene = CJA199; Accession DDBJ/EMBL/GenBank = AF179809

<400> 308

Val Ala Ile Cys His Pro Leu His Tyr Thr Thr Val Met Ser Arg Gly
1 5 10 15

Leu Cys Cys Val Leu Val Ala Ala Ser Trp Met Gly Gly Phe Val His
20 25 30

Ser Thr Val Gln Thr Ile Leu Thr Ile Arg Leu Pro Phe Cys Gly Pro
35 40 45

Asn Gln Val Asp Asn Phe Phe Cys Asp Val Pro Pro Val Ile Lys Leu
50 55 60

Ala Cys Ala Asp Thr Phe Val Ile Glu Leu Leu Met Val Ser Asn Ser
65 70 75 80

Gly Leu Ile Ser Thr Ser Ser Phe Val Val Leu Ile Ser Ser Tyr Thr
85 90 95

Thr Ile Leu Val Lys Ile His Ser Lys Glu Gly Arg Arg Lys Ala Leu
100 105 110

Ser Thr Cys Ala Ser His Leu Met Val Val Thr Leu Phe Gly Pro Cys
115 120 125

Ser Phe Ile Tyr Pro His Pro Phe Ser Thr Phe Ser Val Asp Lys Met
 130 135 140

Val Ser Val Leu Tyr Lys Val Ile Thr Pro Met Leu
 145 150 155

<210> 309
 <211> 488
 <212> DNA
 <213> Callithrix jacchus
 <220>
 <221> misc_feature
 <222> (1)..(488)
 <223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810
 <220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 309
 c gtt gcc att tgc ttc ccc ctt cgc tat atg cta ctc atg agc cat tcc 49
 Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser
 1 5 10 15
 att tgt gtc acg atg att ata gtt tgt tgg tcc att agc ata gct ggg 97
 Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
 20 25 30
 gcc ctg atc ctc act gtc ttc acc atg cat ctg cct tat tgt ggc ccc 145
 Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro
 35 40 45
 tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg 193
 Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
 50 55 60
 gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc atc ttg ggt 241
 Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
 65 70 75 80
 ttc atc ctg ctt ttg gtc cca ctc tcc ctc atc ctg gcc tct tac gtc 289
 Phe Ile Leu Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val
 85 90 95
 ttc atc ttt gcc tct atc ttc aga atc cgc tca gcg cag ggg agg ctc 337
 Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu
 100 105 110
 aag tcc ttc tcc acg tgt gct tcc cac gtc act gtg gtc acc atg ttc 385
 Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
 115 120 125
 tat ggg ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac 433
 Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
 130 135 140
 cca gag cgg gac aag aag cta gcg ctg ttc tac aat gtg gtc tct ggc 481
 Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly
 145 150 155 160

ttc ctc a
Phe Leu

488

<210> 310
<211> 162
<212> PRT
<213> Callithrix jacchus

<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9483; gene = CJA201; Accession DDBJ/EMBL/GenBank = AF179810

<400> 310

Val Ala Ile Cys Phe Pro Leu Arg Tyr Met Leu Leu Met Ser His Ser
1 5 10 15

Ile Cys Val Thr Met Ile Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
20 25 30

Ala Leu Ile Leu Thr Val Phe Thr Met His Leu Pro Tyr Cys Gly Pro
35 40 45

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
50 55 60

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
65 70 75 80

Phe Ile Leu Leu Leu Val Pro Leu Ser Leu Ile Leu Ala Ser Tyr Val
85 90 95

Phe Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Ala Gln Gly Arg Leu
100 105 110

Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
115 120 125

Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
130 135 140

Pro Glu Arg Asp Lys Lys Leu Ala Leu Phe Tyr Asn Val Val Ser Gly
145 150 155 160

Phe Leu

<210> 311
<211> 487
<212> DNA
<213> Callithrix jacchus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 311
 t gtg gca att tgc cac ccc tta cgt tac act gcc aca atg aac ctg cgc 49
 Val Ala Ile Cys His Pro Leu Arg Tyr Thr Ala Thr Met Asn Leu Arg
 1 5 10 15

 ctt tgt gtc cag cta gtg gct gga ctg tgg ctt gtt act tac ctc cat 97
 Leu Cys Val Gln Leu Val Ala Gly Leu Trp Leu Val Thr Tyr Leu His
 20 25 30

 gcc ctc ctg cat act tcc cta ata gca cat ctg tcc ttc tgt gcc ttc 145
 Ala Leu Leu His Thr Ser Leu Ile Ala His Leu Ser Phe Cys Ala Phe
 35 40 45

 aat atc atc cat cat ttc ttc tgt gat ctc aac cct cta cta cgg ctc 193
 Asn Ile Ile His His Phe Phe Cys Asp Leu Asn Pro Leu Leu Arg Leu
 50 55 60

 tct tgc tct gcc gtc tcc ttc aac gta atg atc att ttt gca gta gga 241
 Ser Cys Ser Ala Val Ser Phe Asn Val Met Ile Ile Phe Ala Val Gly
 65 70 75 80

 ggt cta ttg gct ctc acg ccc ctt gtc tgt atc ctc gta ttt tat gga 289
 Gly Leu Leu Ala Leu Thr Pro Leu Val Cys Ile Leu Val Phe Tyr Gly
 85 90 95

 ctt atc ttc tcc act gtt ctg aag atc acc tct act cag ggg aaa cag 337
 Leu Ile Phe Ser Thr Val Leu Lys Ile Thr Ser Thr Gln Gly Lys Gln
 100 105 110

 aga gct gct tcc acc tgc ggc tgc cac ctg tca gta gtg gtg ctg ttt 385
 Arg Ala Ala Ser Thr Cys Gly Cys His Leu Ser Val Val Val Leu Phe
 115 120 125

 tat ggc aca gcc att gcc gtc tac ttt agc ccc tca tcc tcc cat acg 433
 Tyr Gly Thr Ala Ile Ala Val Tyr Phe Ser Pro Ser Ser Ser His Thr
 130 135 140

 cct gag agt gac act ctc tcg acc gtc atg tat tca gtg gtg gcc ccg 481
 Pro Glu Ser Asp Thr Leu Ser Thr Val Met Tyr Ser Val Val Ala Pro
 145 150 155 160

 atg ctg 487
 Met Leu

<210> 312
 <211> 162
 <212> PRT
 <213> Callithrix jacchus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9483; gene = CJA202; Accession DDBJ/EMBL/GenBank = AF179811


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gaccattggc attgggggtgc caattgtcac catTTTTatc tcttatgggtt ttattctttc 300
cagcattctc cacattagct cacagagggc aggtcaggtc taaagccttc agtacctgca 360
gttcccatat aattgtggta tcgcttttct ttgggtcagg tgctttcatg tacctcaaac 420
caccttctct tctacccctg gaccagggga aagtgtcctc catTTTTat actgctgtgg 480
tgcccatggt t 491

<210> 314
<211> 480
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(480)
<223> Taxon = 9600; gene = PPY111; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179813

<400> 314
tgtggccatc tgcttcccc tgcactacac catccatcat gagcccatg ctctgtctct 60
cccttttggc gctgtcctgg gtgctgacca ccttccatgc catgttacac actttactca 120
tggccagggt gtgtttttgt gcagacaatg tgatcccca ctttttctgt gatatgtctg 180
ctctgtgaa gctgtcctgc tctgacactc gagttaatga attggtgata tttatcatgg 240
gagggctcat tcttgtcatc ccattcctac tcctccttgg gtccatgca cgaattgtct 300
cctccatcct caaggctcct tctaagggta tctgcaaggc cttctctact tgtggctccc 360
acctctctgt ggtgtccctg ttctatggga ccgttagtgg tctctactta tgcccatcgg 420
ctaatagttc tactctgaag gagactgtca tggctgtaat gtacactgtg gtgaccccca 480

<210> 315
<211> 486
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814

<220>
<221> CDS
<222> (1)..(486)
<223> Product = olfactory receptor

<400> 315
tgt gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 48
Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1 5 10 15

cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 96
Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20 25 30

gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac 144
Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

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35          40          45
cac atc atc tct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ctg 192
His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50          55          60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga 240
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65          70          75          80

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt 288
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85          90          95

cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc 336
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100         105         110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat 384
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115         120         125

tat ggg aca att att ggt ctc tat ttt cta ccc cca tcc agc aac acc 432
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130         135         140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc 480
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145         150         155         160

atg ttg 486
Met Leu

<210> 316
<211> 162
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9600; gene = PPY112; Accession DDBJ/EMBL/GenBank = AF179814

<400> 316

Cys Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1          5          10          15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
20          25          30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35          40          45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50          55          60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65          70          75          80

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 317
<211> 487
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9600; gene = PPY113; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179815

<400> 317
cactgccatt tgccaccctc taagataaac caatctcatg agacccaaaa tttgtggact 60
tatgactgcc ttctcctgga tcctgggctc tacggatgga atcattgatg ctgcagcgac 120
attttccttc tctactgtg ggtctcggga aatagccac ttcttctgtg agttcccttc 180
catactaadc ctctcatgca atgacacatc aatatttgaa aaggttcttt tcatctgctg 240
tatagtaatg attgtttttc ctgttgcaat catcatcgct tcctatgctc aagttattct 300
ggctgtcatt cacatgggat ctggagaggg tcgtcggata gctttcacga cctgttcctc 360
tcacctcatg gtggtgggaa tgtactatgg agcagctttg ttcattgtaca tacggccac 420
atctgatcgc tcccctacac aggacaagat ggtgtctgta ttctacacca tctcactcc 480
catgctg 487

<210> 318
<211> 484
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

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<220>
<221> CDS
<222> (2)..(484)
<223> product = olfactory receptor

<400> 318
t  gtg gcc atc tgc ttc ccc ctg cac tac acc gcc atc atg agc ccc atg      49
  Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
    1              5              10              15

ctc tgt ctc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat      97
Leu Cys Leu Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
    20              25              30

gcc atg tta cac act tta ctc atg gcc agg ttg tgt ttt tgt gca gac      145
Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Cys Phe Cys Ala Asp
    35              40              45

aat gtg atc ccc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg      193
Asn Val Ile Pro His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
    50              55              60

tcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga      241
Ser Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
    65              70              75              80

ggg ctc att ctt gtc atc cca ttc cta ctc atc ctt ggg tcc tat gca      289
Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Leu Gly Ser Tyr Ala
    85              90              95

cga att gtc tcc tcc atc ctc aag gtc cct tct aag ggt atc tgc aag      337
Arg Ile Val Ser Ser Ile Leu Lys Val Pro Ser Lys Gly Ile Cys Lys
    100             105             110

gcc ttc tct act tgt ggc tcc cac ctc tct gtg gtg tcc ctg ttc tat      385
Ala Phe Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr
    115             120             125

ggg acc gtt agt ggt ctc tac tta tgc cca tcg gct aat agt tct act      433
Gly Thr Val Ser Gly Leu Tyr Leu Cys Pro Ser Ala Asn Ser Ser Thr
    130             135             140

ctg aag gag act gtc atg gct gta atg tac act gtg gtg acc ccc atg      481
Leu Lys Glu Thr Val Met Ala Val Met Tyr Val Val Val Thr Pro Met
    145             150             155             160

ctg
Leu

484

<210> 319
<211> 161
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9600; gene = PPY114; Accession DDBJ/EMBL/GenBank = AF179816

<400> 319
Val Ala Ile Cys Phe Pro Leu His Tyr Thr Ala Ile Met Ser Pro Met
1              5              10              15

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Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Leu Cys His Asn
      35              40              45

gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc      192
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
      50              55              60

tgt gtg gac gtc tcc ttc aac aag gcc atg gtg gcc atc tca ggg ttt      240
Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe
      65              70              75              80

ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac      288
Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
      85              90              95

ata gtt gct gcc att ctt cat att cct tct gcc cag gga cgc cgc aaa      336
Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys
      100             105             110

gcc ttt ggg act tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt      384
Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
      115             120             125

ggg gct aca atg ttc acc tac atg aga cct gcg ggc ggc tcc tcc ctg      432
Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
      130             135             140

gaa aag aag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg      480
Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
      145             150             155             160

ctt
Leu
      483

<210> 321
<211> 161
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(483)
<223> Taxon = 9600; gene = PPY115; Accession DDBJ/EMBL/GenBank = AF179817

<400> 321

Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1              5              10              15

Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
      20              25              30

Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Leu Leu Cys His Asn
      35              40              45

Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
      50              55              60

Cys Val Asp Val Ser Phe Asn Lys Ala Met Val Ala Ile Ser Gly Phe
      65              70              75              80

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Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
85 90 95

Ile Val Ala Ala Ile Leu His Ile Pro Ser Ala Gln Gly Arg Arg Lys
100 105 110

Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
115 120 125

Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
130 135 140

Glu Lys Lys Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
145 150 155 160

Leu

<210> 322
<211> 484
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(484)
<223> Taxon = 9600; gene = PPY116; Accession DDBJ/EMBL/GenBank = AF179818

<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor

<400> 322
t gtg gcc gtc tgc cac cca ctg cat tac acg ctc atc atg cat gga ggg 49
Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
1 5 10 15
ctg tgc ctg ggg ctg gtg gcc ggc tgc ctg gtg gct ggt ttc atg aat 97
Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
20 25 30
tcc ctg atg gaa aca att atc acc ttc cag ctt ccc ctg tgt cac aat 145
Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn
35 40 45
gtt att aat cac ttt gcc tgt gag acc tta gca gtg cta cga cta gcc 193
Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
50 55 60
tgt gtg gac gtc tcc ttc aac aag gcc acg gtg gcc atc tca ggg ttt 241
Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe
65 70 75 80
ctg gtg atc ctg ctt ccc tgt tca ctg atc cta ttc tcc tat gct cac 289
Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
85 90 95

ata gtt gct gcc att ctt cgt att cct tct gcc cag gga cac cgc aaa 337
 Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys
 100 105 110
 gcc ttt ggg acc tgc acg tct cac ctc act gtg gtt tgc atg tgc ttt 385
 Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
 115 120 125
 ggg gct aca atg ttc acc tac atg aga cct gcg ggt ggc tcc tcc ctg 433
 Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu
 130 135 140
 gaa aag gag aat atg gtt gcc ctc ttt tat gcc att gtg att cca atg 481
 Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
 145 150 155 160
 ctt 484
 Leu

<210> 323
 <211> 161
 <212> PRT
 <213> Pongo pygmaeus
 <220>
 <221> misc_feature
 <222> (1)..(484)
 <223> Taxon = 9600; gene = PPY116; Accession DDBJ/EMBL/GenBank = AF179818
 <400> 323

Val Ala Val Cys His Pro Leu His Tyr Thr Leu Ile Met His Gly Gly
 1 5 10 15
 Leu Cys Leu Gly Leu Val Ala Gly Cys Leu Val Ala Gly Phe Met Asn
 20 25 30
 Ser Leu Met Glu Thr Ile Ile Thr Phe Gln Leu Pro Leu Cys His Asn
 35 40 45
 Val Ile Asn His Phe Ala Cys Glu Thr Leu Ala Val Leu Arg Leu Ala
 50 55 60
 Cys Val Asp Val Ser Phe Asn Lys Ala Thr Val Ala Ile Ser Gly Phe
 65 70 75 80
 Leu Val Ile Leu Leu Pro Cys Ser Leu Ile Leu Phe Ser Tyr Ala His
 85 90 95
 Ile Val Ala Ala Ile Leu Arg Ile Pro Ser Ala Gln Gly His Arg Lys
 100 105 110
 Ala Phe Gly Thr Cys Thr Ser His Leu Thr Val Val Cys Met Cys Phe
 115 120 125
 Gly Ala Thr Met Phe Thr Tyr Met Arg Pro Ala Gly Gly Ser Ser Leu

130

135

140

Glu Lys Glu Asn Met Val Ala Leu Phe Tyr Ala Ile Val Ile Pro Met
 145 150 155 160

Leu

<210> 324

<211> 479

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(479)

<223> Taxon = 9600; gene = PPY117; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179819

<400> 324

tgtagccata tgcaaaccct tatactatgt ggatcatcatg agccgaagga cacgcactgt 60
 cttggtaatg atctcctggg ctgtgggctt ggtgcacaca ttaagccagt tatcatttac 120
 tgtgaacctg ccttttttgt ggacctaatg tagtagacag ctttttttgt gatcttcctc 180
 gagtgaccaa acttgccctgc ctggactctt acctcattga aatactaatt gtgggtcaata 240
 gtggagttct ttccctaagc actttctgtc tcttggtcag ctccctacatc attattcttg 300
 ttatggtttg gctcaagtct tcggctgcaa tggcgaaggc attttctacg ctggcttccc 360
 atattgcagt agtaatatta ttctttggac cttgcatctt catctatgtg tggcccttta 420
 ccatctatcc ttgggataaa cttcttgcca tattttacac tgttttcacc cccatccta 479

<210> 325

<211> 487

<212> DNA

<213> Pongo pygmaeus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 325

t gtg gcc atc tgt cac cct cta cat tat gcc acc atc atg agt cag agc 49
 Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
 1 5 10 15
 cag tgt gtc atg ctg gtg gct ggg tcc tgg gtc atc gct tgt gcg tgt 97
 Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
 20 25 30
 gct ctt ttg cat acc ctc ctt ctg gcc cgg ctt tcc ttc tgt gct gac 145
 Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp

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          35              40              45
cac atc atc tct cac ttc ttc tgt gac ctt ggt gcc ctg ctc aag ctg      193
His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
   50              55              60

tcc tgc tca gac acc tcc ctc aat cag tta gca atc ttt aca gca gga      241
Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
   65              70              75

ttg aca gcc att atg ctt cca ttc ctg tgc atc ctg gtt tct tat ggt      289
Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
              85              90              95

cac att ggg gtc acc atc ctc cag att ccc tcc acc aag ggc ata tgc      337
His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
              100              105              110

aaa gcc ttg tcc act tgt gga tcc cac ctc tca gtg gtg act atc tat      385
Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
              115              120              125

tat ggg aca att att ggt ctc tat ttt ctt ccc cca tcc agc aac acc      433
Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
              130              135              140

aat gac aag aac ata att gct tca gtg ata tac aca gta gtc act ccc      481
Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
   145              150              155              160

atg ttg      487
Met Leu

<210> 326
<211> 162
<212> PRT
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9600; gene = PPY118; Accession DDBJ/EMBL/GenBank = AF179820

<400> 326

Val Ala Ile Cys His Pro Leu His Tyr Ala Thr Ile Met Ser Gln Ser
1              5              10              15

Gln Cys Val Met Leu Val Ala Gly Ser Trp Val Ile Ala Cys Ala Cys
              20              25              30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
              35              40              45

His Ile Ile Ser His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
   50              55              60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
   65              70              75              80

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Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 327
<211> 475
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(475)
<223> Taxon = 9600; gene = PPY119; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179821

<400> 327
gtagccataa gcaaacctct ccactatgca atcatcatga actcatgcac atgtacaggc 60
ccagtggttag gctcttgggt cattgggggt atgcactccc tgagccagtt agctttcact 120
gtaagcttgc ccttctgtgg ccacaaacata gtggacagtt attattgcga ccttactttg 180
gtcatcaaac gtgcctgtac agatgcttat atccctgaag tgttgatgct tttggacggg 240
ggctttatgg gggtgacctat ttttgctttt gctgatctcc tacacgggtca ttctgattac 300
tgtgcagcga cattcctcag caggatatggc caaggctcac agcactctga ctgcccacat 360
tgctgtggtg accgtgttct ttgggccttg tatcttcac tatgcctggc ctttcagcaa 420
cttaccagtg gataacattt tgtctgtatt ctctgtagtt ttcacaccta tatta 475

<210> 328
<211> 487
<212> DNA
<213> Pongo pygmaeus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9600; gene = PPY120; Accession DDBJ/EMBL/GenBank = AF179822

<220>
<221> CDS

20

25

30

Ala Leu Leu His Thr Leu Leu Leu Ala Arg Leu Ser Phe Cys Ala Asp
35 40 45

His Ile Ile Pro His Phe Phe Cys Asp Leu Gly Ala Leu Leu Lys Leu
50 55 60

Ser Cys Ser Asp Thr Ser Leu Asn Gln Leu Ala Ile Phe Thr Ala Gly
65 70 75 80

Leu Thr Ala Ile Met Leu Pro Phe Leu Cys Ile Leu Val Ser Tyr Gly
85 90 95

His Ile Gly Val Thr Ile Leu Gln Ile Pro Ser Thr Lys Gly Ile Cys
100 105 110

Lys Ala Leu Ser Thr Cys Gly Ser His Leu Ser Val Val Thr Ile Tyr
115 120 125

Tyr Gly Thr Ile Ile Gly Leu Tyr Phe Leu Pro Pro Ser Ser Asn Thr
130 135 140

Asn Asp Lys Asn Ile Ile Ala Ser Val Ile Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 330

<211> 487

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 330

t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg 49
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc 97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20 25 30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg cct ttc tgt gat gca 145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala
35 40 45

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aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
   50                               55                               60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
   65                               70                               75                               80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
                               85                               90                               95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
                               100                               105                               110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
                               115                               120                               125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
                               130                               135                               140

att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
   145                               150                               155                               160

atg ctg      487
Met Leu

<210> 331
<211> 162
<212> PRT
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC184; Accession DDBJ/EMBL/GenBank = AF179823

<400> 331

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1                               5                               10                               15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20                               25                               30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Pro Phe Cys Asp Ala
35                               40                               45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50                               55                               60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65                               70                               75                               80

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Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
145 150 155 160

Met Leu

<210> 332
<211> 488
<212> DNA
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 9521; gene = SSC185; Accession DDBJ/EMBL/GenBank = AF179824

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 332
t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg 49
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1 5 10 15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc 97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20 25 30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca 145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
35 40 45

aac acc gtc cac cac tac ttc tgt gac ctt gct gcc ctg ctc aag ctg 193
Asn Thr Val His His Tyr Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50 55 60

tcc tgc tca gat atc ttc ctc aac gag ctg gtc atg ttc aca gta ggg 241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65 70 75 80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc 289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85 90 95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc 337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg

Parameter	Value	Unit
Mean	1.0	
Standard deviation	0.5	
Minimum	0.0	
Maximum	2.0	
Range	2.0	
Skewness	0.0	
Kurtosis	0.0	
Mode	1.0	
Median	1.0	
Interquartile range	1.0	
90th percentile	1.5	
10th percentile	0.5	
5th percentile	0.0	
95th percentile	2.0	
99th percentile	2.0	
1st percentile	0.0	
25th percentile	0.5	
75th percentile	1.5	
Mean absolute deviation	0.5	
Geometric mean	1.0	
Harmonic mean	1.0	
Weighted mean	1.0	
Weighted standard deviation	0.5	
Weighted minimum	0.0	
Weighted maximum	2.0	
Weighted range	2.0	
Weighted skewness	0.0	
Weighted kurtosis	0.0	
Weighted mode	1.0	
Weighted median	1.0	
Weighted interquartile range	1.0	
Weighted 90th percentile	1.5	
Weighted 10th percentile	0.5	
Weighted 5th percentile	0.0	
Weighted 95th percentile	2.0	
Weighted 99th percentile	2.0	
Weighted 1st percentile	0.0	
Weighted 25th percentile	0.5	
Weighted 75th percentile	1.5	
Weighted mean absolute deviation	0.5	
Weighted geometric mean	1.0	
Weighted harmonic mean	1.0	
Weighted weighted mean	1.0	
Weighted weighted standard deviation	0.5	
Weighted weighted minimum	0.0	
Weighted weighted maximum	2.0	
Weighted weighted range	2.0	
Weighted weighted skewness	0.0	
Weighted weighted kurtosis	0.0	
Weighted weighted mode	1.0	
Weighted weighted median	1.0	
Weighted weighted interquartile range	1.0	
Weighted weighted 90th percentile	1.5	
Weighted weighted 10th percentile	0.5	
Weighted weighted 5th percentile	0.0	
Weighted weighted 95th percentile	2.0	
Weighted weighted 99th percentile	2.0	
Weighted weighted 1st percentile	0.0	
Weighted weighted 25th percentile	0.5	
Weighted weighted 75th percentile	1.5	
Weighted weighted mean absolute deviation	0.5	
Weighted weighted geometric mean	1.0	
Weighted weighted harmonic mean	1.0	
Weighted weighted weighted mean	1.0	
Weighted weighted weighted standard deviation	0.5	
Weighted weighted weighted minimum	0.0	
Weighted weighted weighted maximum	2.0	
Weighted weighted weighted range	2.0	
Weighted weighted weighted skewness	0.0	
Weighted weighted weighted kurtosis	0.0	
Weighted weighted weighted mode	1.0	
Weighted weighted weighted median	1.0	
Weighted weighted weighted interquartile range	1.0	
Weighted weighted weighted 90th percentile	1.5	
Weighted weighted weighted 10th percentile	0.5	
Weighted weighted weighted 5th percentile	0.0	
Weighted weighted weighted 95th percentile	2.0	
Weighted weighted weighted 99th percentile	2.0	
Weighted weighted weighted 1st percentile	0.0	
Weighted weighted weighted 25th percentile	0.5	
Weighted weighted weighted 75th percentile	1.5	
Weighted weighted weighted mean absolute deviation	0.5	
Weighted weighted weighted geometric mean	1.0	
Weighted weighted weighted harmonic mean	1.0	
Weighted weighted weighted weighted mean	1.0	
Weighted weighted weighted weighted standard deviation	0.5	
Weighted weighted weighted weighted minimum	0.0	
Weighted weighted weighted weighted maximum	2.0	
Weighted weighted weighted weighted range	2.0	
Weighted weighted weighted weighted skewness	0.0	
Weighted weighted weighted weighted kurtosis	0.0	
Weighted weighted weighted weighted mode	1.0	
Weighted weighted weighted weighted median	1.0	
Weighted weighted weighted weighted interquartile range	1.0	
Weighted weighted weighted weighted 90th percentile	1.5	
Weighted weighted weighted weighted 10th percentile	0.5	
Weighted weighted weighted weighted 5th percentile	0.0	
Weighted weighted weighted weighted 95th percentile	2.0	
Weighted weighted weighted weighted 99th percentile	2.0	
Weighted weighted weighted weighted 1st percentile	0.0	
Weighted weighted weighted weighted 25th percentile	0.5	
Weighted weighted weighted weighted 75th percentile	1.5	
Weighted weighted weighted weighted mean absolute deviation	0.5	
Weighted weighted weighted weighted geometric mean	1.0	
Weighted weighted weighted weighted harmonic mean	1.0	
Weighted weighted weighted weighted weighted mean	1.0	
Weighted weighted weighted weighted weighted standard deviation	0.5	
Weighted weighted weighted weighted weighted minimum	0.0	
Weighted weighted weighted weighted weighted maximum	2.0	
Weighted weighted weighted weighted weighted range	2.0	
Weighted weighted weighted weighted weighted skewness	0.0	
Weighted weighted weighted weighted weighted kurtosis	0.0	
Weighted weighted weighted weighted weighted mode	1.0	
Weighted weighted weighted weighted weighted median	1.0	
Weighted weighted weighted weighted weighted interquartile range	1.0	
Weighted weighted weighted weighted weighted 90th percentile	1.5	
Weighted weighted weighted weighted weighted 10th percentile	0.5	
Weighted weighted weighted weighted weighted 5th percentile	0.0	
Weighted weighted weighted weighted weighted 95th percentile	2.0	
Weighted weighted weighted weighted weighted 99th percentile	2.0	
Weighted weighted weighted weighted weighted 1st percentile	0.0	
Weighted weighted weighted weighted weighted 25th percentile	0.5	

Val	Ala	Ile	Cys	Tyr	Pro	Leu	His	Tyr	Thr	Ala	Ile	Met	Arg	Glu	Gly
1				5					10					15	
Leu	Cys	Ala	Phe	Leu	Val	Ala	Val	Ser	Trp	Ile	Pro	Ser	Cys	Ala	Ser
			20					25					30		
Ser	Leu	Ser	His	Thr	Leu	Leu	Leu	Thr	Pro	Leu	Ser	Phe	Cys	Asp	Ala
		35					40					45			
Asn	Thr	Val	His	His	Tyr	Phe	Cys	Asp	Leu	Ala	Ala	Leu	Leu	Lys	Leu
	50					55					60				
Ser	Cys	Ser	Asp	Ile	Phe	Leu	Asn	Glu	Leu	Val	Met	Phe	Thr	Val	Gly
65					70					75					80
Val	Val	Val	Ile	Thr	Leu	Pro	Phe	Met	Cys	Ile	Leu	Val	Ser	Tyr	Gly
				85					90					95	
Tyr	Thr	Gly	Ala	Thr	Ile	Leu	Arg	Val	Pro	Ser	Thr	Lys	Gly	Ile	Arg
			100					105					110		
Lys	Ala	Leu	Ser	Met	Cys	Gly	Ser	Arg	Leu	Ser	Val	Val	Ser	Leu	Tyr
		115					120					125			
Tyr	Gly	Ser	Ile	Phe	Gly	Gln	Tyr	Leu	Phe	Pro	Thr	Val	Ser	Ser	Ser
	130					135					140				

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 334
 <211> 487
 <212> DNA
 <213> Saimiri sciureus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 334
 t gtg gcc act tgt cac ccc ctt aga tac atg gtc atc atg aac ccc tgc 49
 Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
 1 5 10 15
 ctc tgc agc ctg ctg att ctt ctt tct ccg ttg act agc gtt gtg aat 97
 Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
 20 25 30
 gcc ctt ctt ctc agc ctg atg gtg ttg agg ctg tcc ttc tgc aca gat 145
 Ala Leu Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
 35 40 45
 ctg gaa atc ccg ctc ttc ttc tgt gaa ctg gct cag gtc atc cag ctt 193
 Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
 50 55 60
 gct tgt tct gac acc ctc atc aat aac atc ctg ata tat ttt gca gct 241
 Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
 65 70 75 80
 tgc ata ttt ggt ggt gtt cct ctg tct gga atc ata ttc tct tat gct 289
 Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
 85 90 95
 cag att gcc tcc tct att ttg aga atg cca tca gca cgc aga aag tat 337
 Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
 100 105 110
 aaa gcc ttt tcc acc tgt ggg tct cac ctc tcc atg gtg ctc ttg ttc 385
 Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
 115 120 125
 tat agg aca ggt ttg ggg gtg tac att agt tct gca gtt act gac tca 433
 Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
 130 135 140
 cct agg aag act gca gtg gct tca atg atg tat tct gtg ggt cct caa 481
 Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
 145 150 155 160
 atg gtg 487

Met Val

<210> 335
<211> 162
<212> PRT
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC186; Accession DDBJ/EMBL/GenBank = AF179825

<400> 335

Val Ala Thr Cys His Pro Leu Arg Tyr Met Val Ile Met Asn Pro Cys
1 5 10 15

Leu Cys Ser Leu Leu Ile Leu Leu Ser Pro Leu Thr Ser Val Val Asn
20 25 30

Ala Leu Leu Leu Ser Leu Met Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

Leu Glu Ile Pro Leu Phe Phe Cys Glu Leu Ala Gln Val Ile Gln Leu
50 55 60

Ala Cys Ser Asp Thr Leu Ile Asn Asn Ile Leu Ile Tyr Phe Ala Ala
65 70 75 80

Cys Ile Phe Gly Gly Val Pro Leu Ser Gly Ile Ile Phe Ser Tyr Ala
85 90 95

Gln Ile Ala Ser Ser Ile Leu Arg Met Pro Ser Ala Arg Arg Lys Tyr
100 105 110

Lys Ala Phe Ser Thr Cys Gly Ser His Leu Ser Met Val Leu Leu Phe
115 120 125

Tyr Arg Thr Gly Leu Gly Val Tyr Ile Ser Ser Ala Val Thr Asp Ser
130 135 140

Pro Arg Lys Thr Ala Val Ala Ser Met Met Tyr Ser Val Gly Pro Gln
145 150 155 160

Met Val

<210> 336
<211> 487
<212> DNA
<213> Saimiri sciureus

<220>

Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
1 5 10 15

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

Ala Met Leu His Thr Leu Leu Met Ala Arg Leu Arg Phe Cys Ala Asp
35 40 45

Asn Val Ile Leu His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
145 150 155 160

Met Leu

<210> 338
<211> 487
<212> DNA
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC190; Accession DDBJ/EMBL/GenBank = AF179827

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 338
t gtg gcc atc tgt aag ccc ctg cat tac acc acc atc atg agc agc aaa 49
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc 97

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Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
      20                      25                      30

atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gcc tcc      145
Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
      35                      40                      45

aac gtc gtt gat cat ttc tac ttt gac act atc ccg ctc ctg cag att      193
Asn Val Val Asp His Phe Tyr Phe Asp Thr Ile Pro Leu Leu Gln Ile
      50                      55                      60

tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tca gcg      241
Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
      65                      70                      75                      80

ttg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca tat act      289
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
      85                      90                      95

tat att gcc ctg aca att cta aaa atc cct tca act agt cag agg aaa      337
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
      100                      105                      110

aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ctt tct      385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
      115                      120                      125

tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa caa agg      433
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
      130                      135                      140

gta tct ttt tca aag gga att tgc gtg ctc aat acc tct gtt gct cca      481
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
      145                      150                      155                      160

ctt ttg
Leu Leu
      487

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<210> 339
<211> 162
<212> PRT
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC190; Accession DDBJ/EMBL/GenBank = AF179827

<400> 339

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Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1          5          10          15

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Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
      20                      25                      30

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Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
      35                      40                      45

```

```

Asn Val Val Asp His Phe Tyr Phe Asp Thr Ile Pro Leu Leu Gln Ile
      50                      55                      60

```

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
65 70 75 80

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
85 90 95

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
130 135 140

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
145 150 155 160

Leu Leu

<210> 340

<211> 485

<212> DNA

<213> Saimiri sciureus

<220>

<221> misc_feature

<222> (1)..(485)

<223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF179828

<220>

<221> CDS

<222> (1)..(483)

<223> Product = olfactory receptor

<400> 340

gtg gcc att tgc cac cct ctt caa tac tca gtc atc atg acc aca ggt 48
Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
1 5 10 15

tac tgt gga cag ctg gtg gct ttc tct tac atg agt ggt ttc atg atc 96
Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
20 25 30

tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc 144
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
35 40 45

aat gtt atg aac cac ttt ttc tgt gat atc tca cca gtc cta aaa ctg 192
Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
50 55 60

gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct 240
Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
65 70 75 80

atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc 288
 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
 85 90 95
 tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag 336
 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
 100 105 110
 aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt 384
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
 115 120 125
 tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca 432
 Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
 130 135 140
 ttt aat tcc aac aaa cta atg tca gct gtg tat gca gtc ctc aca ccc 480
 Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro
 145 150 155 160
 atg ct 485
 Met

<210> 341
 <211> 161
 <212> PRT
 <213> Saimiri sciureus

<220>
 <221> misc_feature
 <222> (1)..(485)
 <223> Taxon = 9521; gene = SSC191; Accession DDBJ/EMBL/GenBank = AF179828
 <400> 341

Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly
 1 5 10 15
 Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile
 20 25 30
 Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser
 35 40 45
 Asn Val Met Asn His Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu
 50 55 60
 Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
 65 70 75 80
 Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
 85 90 95
 Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
 100 105 110
 Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe


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115              120              125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
130              135              140

Phe Asn Ser Asn Lys Leu Met Ser Ala Val Tyr Ala Val Leu Thr Pro
145              150              155              160

Met

<210> 342
<211> 487
<212> DNA
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC192; Accession DDBJ/EMBL/GenBank = AF179829

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 342
t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg      49
Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
1              5              10              15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc      97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
20              25              30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca      145
Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
35              40              45

aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
50              55              60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
65              70              75

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
85              90              95

tac act ggg gcc act atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
100              105              110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
115              120              125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
130              135              140

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att gac aag gat gtc att gtg gct cta atg tac aca gtg gtc aca ccc 481
 ile asp lys asp val ile val ala leu met tyr thr val val thr pro
 145 150 155 160

atg ctg 487
 met leu

<210> 343
 <211> 162
 <212> PRT
 <213> Saimiri sciureus

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9521; gene = SSC192; Accession DDBJ/EMBL/GenBank = AF179829

<400> 343

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
 1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

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<210> 344
<211> 487
<212> DNA
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 344
t gtt gcc ata tgt tac cct ctc cac tac act gcc atc atg agg gaa ggg      49
  Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
    1             5             10             15

ctc tgt gcc ttc tta gtg gct gta tct tgg att cca tct tgt gct agc      97
Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
          20             25             30

tcc ctc tct cac acc ctt ctg ctg acc ccg ctg tct ttc tgt gat gca      145
Ser Leu Ser His Thr Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
          35             40             45

aac acc gtc cac cac ttc ttc tgt gac ctt gct gcc ctg ctc aag ctg      193
Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
          50             55             60

tcc tgc tca gat atc ttc ctc aat gag ctg gtc atg ttc aca gta ggg      241
Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
        65             70             75             80

gtg gtg gtc att acc ctg cca ttc atg tgt atc ctg gta tca tat ggc      289
Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
          85             90             95

tac act ggg gcc acc atc ctg agg gtc cct tca acc aaa ggg atc cgc      337
Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
          100            105            110

aaa gcg ttg tcc atg tgt ggc tcc cgt ctc tct gtg gtg tct ctg tat      385
Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
          115            120            125

tat ggc tca ata ttt ggc cag tac ctt ttc cca act gta agc agt tcc      433
Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
          130            135            140

att gac aag gat gtc att gtg gct cta acg tac aca gtg gtc aca ccc      481
Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
          145            150            155            160

atg ctg      487
Met Leu

<210> 345
<211> 162
<212> PRT
<213> Saimiri sciureus

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0045150001

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 9521; gene = SSC193; Accession DDBJ/EMBL/GenBank = AF179830
 <400> 345

Val Ala Ile Cys Tyr Pro Leu His Tyr Thr Ala Ile Met Arg Glu Gly
 1 5 10 15

Leu Cys Ala Phe Leu Val Ala Val Ser Trp Ile Pro Ser Cys Ala Ser
 20 25 30

Ser Leu Ser His Thr Leu Leu Leu Thr Pro Leu Ser Phe Cys Asp Ala
 35 40 45

Asn Thr Val His His Phe Phe Cys Asp Leu Ala Ala Leu Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Ile Phe Leu Asn Glu Leu Val Met Phe Thr Val Gly
 65 70 75 80

Val Val Val Ile Thr Leu Pro Phe Met Cys Ile Leu Val Ser Tyr Gly
 85 90 95

Tyr Thr Gly Ala Thr Ile Leu Arg Val Pro Ser Thr Lys Gly Ile Arg
 100 105 110

Lys Ala Leu Ser Met Cys Gly Ser Arg Leu Ser Val Val Ser Leu Tyr
 115 120 125

Tyr Gly Ser Ile Phe Gly Gln Tyr Leu Phe Pro Thr Val Ser Ser Ser
 130 135 140

Ile Asp Lys Asp Val Ile Val Ala Leu Thr Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 346
 <211> 486
 <212> DNA
 <213> Saimiri sciureus

<220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 9521; gene = SSC194; Accession DDBJ/EMBL/GenBank = AF179831

<220>
 <221> CDS
 <222> (2)..(484)
 <223> Product = olfactory receptor

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<400> 346
t gtg gcc atc tgt cac ccc ctg cac tac aca gtc acc att aac ccc aga      49
  Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
    1             5             10             15

ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat      97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
      20             25             30

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac      145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
      35             40             45

ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt      193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
      50             55             60

gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct      241
Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
      65             70             75             80

atg ctg ctg ggc ggt ggt ccc ctc aca gga att att tac tct tac tct      289
Met Leu Leu Gly Gly Gly Pro Leu Thr Gly Ile Ile Tyr Ser Tyr Ser
      85             90             95

aag ata gtt tcc tcc ata cgt gca atc tca tca gct cag ggg aag tac      337
Lys Ile Val Ser Ser Ile Arg Ala Ile Ser Ser Ala Gln Gly Lys Tyr
      100            105            110

aag gcg ttt tcc acc tgt gca tct cac atc tta att gtc tcc tta ttt      385
Lys Ala Phe Ser Thr Cys Ala Ser His Ile Leu Ile Val Ser Leu Phe
      115            120            125

tat ggt aca ctc cta ggt gtg tac att agt tct gct gca act ggc aac      433
Tyr Gly Thr Leu Leu Gly Val Tyr Ile Ser Ser Ala Ala Thr Gly Asn
      130            135            140

tca cat tca agt gct gca gcc ttg gtg atg tac act gtg gtc acc ccc      481
Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
      145            150            155            160

atg ct
Met
      486

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```

<210> 347
<211> 161
<212> PRT
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 9521; gene = SSC194; Accession DDBJ/EMBL/GenBank = AF179831

<400> 347

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Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
 1             5             10             15

Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
 20             25             30

```



```

      50              55              60
tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg      241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
65              70              75              80

gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt      289
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
85              90              95

ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
100             105             110

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
115             120             125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
130             135             140

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg ccc      481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
145             150             155             160

atg ttt      487
Met Phe

<210> 349
<211> 162
<212> PRT
<213> Saimiri sciureus

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 9521; gene = SSC195; Accession DDBJ/EMBL/GenBank = AF179832

<400> 349

Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1              5              10              15

Val Cys Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
20             25             30

Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
35             40             45

Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
50             55             60

Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
65             70             75             80

Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
85             90             95

```

Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
 115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
 130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
 145 150 155 160

Met Phe

<210> 350
 <211> 486
 <212> DNA
 <213> Saimiri boliviensis

<220>
 <221> misc_feature
 <222> (1)..(486)
 <223> Taxon = 27679; gene = SBO213; pseudogene; Accession DDBJ/EMBL/GenBank
 = AF179833

<400> 350
 cgtggccatc tgccaccctc tccactatcc catccgcatg agtagaagtg tgtgtgtgaa 60
 gatgattgga ggctcttgga cgctgggggc catcaactcc ttggcacaca cagtctatgc 120
 cctccatatt ccctactgca ggtctagagc cattgacatc ttcttctgcg acatcccagc 180
 catgttgctt ctgcctgta cggacacttg ggtctatgaa tacatgggtt ttctaagtac 240
 aagctgcctt ctctcttttc tttccttggc atcacgcgtt cctatggccg agtcctatct 300
 gctgtctacc atacgcattc aaaaaagggg agaaaaaagg cctccaccac catttcaacc 360
 catttaactg tagtgatctt ttactatgca ccttttgtct acacctatct tcggcccagg 420
 aatctccact caccatccga agacaagatc ctggcagtct tctacaccat ccttaccctt 480
 atgctc 486

<210> 351
 <211> 487
 <212> DNA
 <213> Saimiri boliviensis

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO214; Accession DDBJ/EMBL/GenBank = AF179834

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor


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<400> 351
t gtg gcc atc tgt aag ccc ctg cat tac acc acc atc atg agc agc aaa 49
Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

atc tgc ctg cag ctt gtg ctt ggg tgc tgg gtt ctt ggt ttt ctc atc 97
Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
20 25 30

atc ttt cca cca ctc ctc tta gga cta aat ctt gac ttc tgt gcc tcc 145
Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
35 40 45

aac gtc gtt gat cat ttc tac tgt gac act atc ccg ctc ctg cag att 193
Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile
50 55 60

tcc tgc aca gac acg cag ctc ctg gag agg atg gga ttc atc tca gcg 241
Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
65 70 75 80

ctg gtg aca ctc tta gtc aca ttg gta atg gtg ata ata tca tat act 289
Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
85 90 95

tat att gcc ctg aca att cta aaa atc cct tca act agt cag agg aaa 337
Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
100 105 110

aag gct ttt tcc acg tgt tct tct cac atg att gtg ata tcc ctt tct 385
Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
115 120 125

tat ggc agc tgc atc ttc atg tat gtt aag cca tca gtc aaa caa agg 433
Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
130 135 140

gta tct ttt tca aag gga att tcg gtg ctc aat acc tct gtt gct cca 481
Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
145 150 155 160

ctt ttg 487
Leu Leu

```

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<210> 352
<211> 162
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO214; Accession DDBJ/EMBL/GenBank = AF179834

```

```

<400> 352

Val Ala Ile Cys Lys Pro Leu His Tyr Thr Thr Ile Met Ser Ser Lys
1 5 10 15

Ile Cys Leu Gln Leu Val Leu Gly Cys Trp Val Leu Gly Phe Leu Ile
20 25 30

```

Ile Phe Pro Pro Leu Leu Leu Gly Leu Asn Leu Asp Phe Cys Ala Ser
 35 40 45

Asn Val Val Asp His Phe Tyr Cys Asp Thr Ile Pro Leu Leu Gln Ile
 50 55 60

Ser Cys Thr Asp Thr Gln Leu Leu Glu Arg Met Gly Phe Ile Ser Ala
 65 70 75 80

Leu Val Thr Leu Leu Val Thr Leu Val Met Val Ile Ile Ser Tyr Thr
 85 90 95

Tyr Ile Ala Leu Thr Ile Leu Lys Ile Pro Ser Thr Ser Gln Arg Lys
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Met Ile Val Ile Ser Leu Ser
 115 120 125

Tyr Gly Ser Cys Ile Phe Met Tyr Val Lys Pro Ser Val Lys Gln Arg
 130 135 140

Val Ser Phe Ser Lys Gly Ile Ser Val Leu Asn Thr Ser Val Ala Pro
 145 150 155 160

Leu Leu

<210> 353

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 353

c gtt gcc att tgc ttc ccc ctt cac tat acg cta ctc atg agc cat tcc 49
 Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
 1 5 10 15

att tgt gtc aac acg gtc att gtc tgt tgg tcc att agc ata gct ggg 97
 Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
 20 25 30

gcc ctg atc tac act gtc ttc acc ttg cat ctg cct tat tgt ggc ccc 145
 Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
 35 40 45

tac aag ata aac cac ttc ttc tgt gag gtc cct gct gtc ctg aag ttg 193

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Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
  50                      55                      60

gcc tgt gca gac aca tct ttt aat gac agg ctg gac ttc att ttg ggt      241
Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
  65                      70                      75                      80

ttc ctc ctg ctt ttg gtc cca ctc tcc ttc atc ctg gcc tct tac gta      289
Phe Leu Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val
                      85                      90                      95

ctc atc ttt gcc tct atc ttc aga atc cgc tca gtg cag ggg agg ctc      337
Leu Ile Phe Ala Ser Ile Phe Arg Ile Arg Ser Val Gln Gly Arg Leu
                      100                      105                      110

aag tcc ttc tcc acg tgt gct tcc cac gtc act gtg gtc acc atg ttc      385
Lys Ser Phe Ser Thr Cys Ala Ser His Val Thr Val Val Thr Met Phe
                      115                      120                      125

tac gga ccg gcc atc atc atg tac atg agg ccc ggt tct tgg tat gac      433
Tyr Gly Pro Ala Ile Ile Met Tyr Met Arg Pro Gly Ser Trp Tyr Asp
                      130                      135                      140

cca gag tgg gac aag aag gta gag gtg ttg tac aat gtc atc tct gcc      481
Pro Glu Trp Asp Lys Lys Val Glu Val Leu Tyr Asn Val Ile Ser Ala
                      145                      150                      155                      160

ttc ttg
Phe Leu
                                         487

<210> 354
<211> 162
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO215; Accession DDBJ/EMBL/GenBank = AF179835

<400> 354

Val Ala Ile Cys Phe Pro Leu His Tyr Thr Leu Leu Met Ser His Ser
  1                      5                      10                      15

Ile Cys Val Asn Thr Val Ile Val Cys Trp Ser Ile Ser Ile Ala Gly
                      20                      25                      30

Ala Leu Ile Tyr Thr Val Phe Thr Leu His Leu Pro Tyr Cys Gly Pro
                      35                      40                      45

Tyr Lys Ile Asn His Phe Phe Cys Glu Val Pro Ala Val Leu Lys Leu
  50                      55                      60

Ala Cys Ala Asp Thr Ser Phe Asn Asp Arg Leu Asp Phe Ile Leu Gly
  65                      70                      75                      80

Phe Leu Leu Leu Leu Val Pro Leu Ser Phe Ile Leu Ala Ser Tyr Val
                      85                      90                      95

```


Val Thr Thr Asp Arg Ile Leu Ser Leu Phe Tyr Thr Val Ile Thr Pro
 145 150 155 160

Met Leu

<210> 357
 <211> 487
 <212> DNA
 <213> Saimiri boliviensis

<220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AF179837

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 357
 t gtg gcc att tgc cac ccc ctc tac tac tcc aca gtc atg agc ccc caa 49
 Val Ala Ile Cys His Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
 1 5 10 15
 gtc tgt gcc cta atc ctc gtg ttg tgc tgg gtc ctc acc aac gtt gtt 97
 Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val
 20 25 30
 gcc ttg acc cac aca ctc ctc atg gct cga ctg tcc ttc tgt gtg act 145
 Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45
 ggg gaa att gct cac ttt ttc tgt gac atc act cct gtc ctg aag cta 193
 Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60
 tca tgt tct gac acc cac atc aat gag atg atg gtt ttt gtc ttg gga 241
 Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80
 ggc aca gta ctc atc atc ccc ttt cta tgc att gtc acc tcc tac atc 289
 Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
 85 90 95
 tac att gtg cct gct att ctg agg gtc cga acc cat ggt ggg gcg ggc 337
 Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
 100 105 110
 aag gcc ttt tcc acc tgc agt tcc cac ctc tgc att gtt tgt gtg ttc 385
 Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
 115 120 125
 tat ggg acc ctc ttc agt gcc tac ctg tgt cct ccc tcc atc gcc tct 433
 Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
 130 135 140
 gaa gat aag gac att gca aca gct gca atg tat acc ata gtg act ccc 481
 Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
 145 150 155 160
 acg ttg 487
 Thr Leu

<210> 358
 <211> 162
 <212> PRT
 <213> Saimiri boliviensis

 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO217; Accession DDBJ/EMBL/GenBank = AF179837

 <400> 358

Val Ala Ile Cys His Pro Leu Tyr Tyr Ser Thr Val Met Ser Pro Gln
 1 5 10 15

Val Cys Ala Leu Ile Leu Val Leu Cys Trp Val Leu Thr Asn Val Val
 20 25 30

Ala Leu Thr His Thr Leu Leu Met Ala Arg Leu Ser Phe Cys Val Thr
 35 40 45

Gly Glu Ile Ala His Phe Phe Cys Asp Ile Thr Pro Val Leu Lys Leu
 50 55 60

Ser Cys Ser Asp Thr His Ile Asn Glu Met Met Val Phe Val Leu Gly
 65 70 75 80

Gly Thr Val Leu Ile Ile Pro Phe Leu Cys Ile Val Thr Ser Tyr Ile
 85 90 95

Tyr Ile Val Pro Ala Ile Leu Arg Val Arg Thr His Gly Gly Ala Gly
 100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Leu Cys Ile Val Cys Val Phe
 115 120 125

Tyr Gly Thr Leu Phe Ser Ala Tyr Leu Cys Pro Pro Ser Ile Ala Ser
 130 135 140

Glu Asp Lys Asp Ile Ala Thr Ala Ala Met Tyr Thr Ile Val Thr Pro
 145 150 155 160

Thr Leu

<210> 359
 <211> 486
 <212> DNA
 <213> Saimiri boliviensis

 <220>
 <221> misc_feature

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<222> (1)..(486)
<223> Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838

<220>
<221> CDS
<222> (2)..(484)
<223> Product = olfactory receptor

<400> 359
c gtg gct atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag      49
  Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
    1             5             10             15

gtg tgc ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg      97
Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
    20             25             30

gct gtg gct cat atg gga aac ata atg ttt atg acc ttt tgt tca gaa      145
Ala Val Ala His Met Gly Asn Ile Met Phe Met Thr Phe Cys Ser Glu
    35             40             45

aat ctt gtc aat cac tac atg tgt gat gtc ctt ccc ctc ctt gag ctc      193
Asn Leu Val Asn His Tyr Met Cys Asp Val Leu Pro Leu Leu Glu Leu
    50             55             60

tcc tgc aac agc tct tac ata aat ttg ctg ttg gtt ttt att att gtg      241
Ser Cys Asn Ser Ser Tyr Ile Asn Leu Leu Leu Val Phe Ile Ile Val
    65             70             75             80

gcc att ggc att ggg gtg cca att gtc acc att ttt atc tct tat ggt      289
Ala Ile Gly Ile Gly Val Pro Ile Val Thr Ile Phe Ile Ser Tyr Gly
    85             90             95

ttt att ctt tcc agc att ctc cac att agc tcc aca gag ggc agg tct      337
Phe Ile Leu Ser Ser Ile Leu His Ile Ser Ser Thr Glu Gly Arg Ser
   100             105             110

aaa gcc ttc agt acc tgc agc tcc cac ata att gtg gta tcg ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Val Val Ser Leu Phe
   115             120             125

ttt ggg tca gga gct ttt atg tac ctc aaa cca cct tct att cta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Pro Ser Ile Leu Pro
   130             135             140

ctg gac cag ggg aaa gtg tct tcc att ttt tat act gca gtg gtg cca      481
Leu Asp Gln Gly Lys Val Ser Ser Ile Phe Tyr Thr Ala Val Val Pro
   145             150             155             160

tgt tt
Cys
                                         486

<210> 360
<211> 161
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(486)
<223> Taxon = 27679; gene = SBO218; Accession DDBJ/EMBL/GenBank = AF179838

<400> 360

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20	25	30	
tct gtc atc aag gtc tat ttc att tca cat gtt gct ttc tgt ggc tcc			145
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser			
35	40	45	
aat gtt atg aac ctc ttt ttc tgt gat atc tca cca gtc cta aaa ctg			193
Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu			
50	55	60	
gca tgc aaa gac atg tcc aca gct gag cta gtg gac ttt gct tta gct			241
Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala			
65	70	75	80
atc gtc att ctt gtg atc cct ctc att acc act atc ctc tcc tat atc			289
Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile			
85	90	95	
tac att gtc tcc gcc att ctg cat ata ccc tcc acc cag gga agg aag			337
Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys			
100	105	110	
aag gcc ttc tcc acc tgt gca tct cac ctc act gta gtc ata att ttt			385
Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe			
115	120	125	
tac aca gcc atg att ttt aca tat gtt cgg ccc aga gct att gca tca			433
Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser			
130	135	140	
ttt aat tcc aac aaa cta atc tca gct gtc tat gca gtc ctc aca ccc			481
Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro			
145	150	155	160
atg cta			487
Met Leu			
<210>	362		
<211>	162		
<212>	PRT		
<213>	Saimiri boliviensis		
<220>			
<221>	misc_feature		
<222>	(1)..(487)		
<223>	Taxon = 27679; gene = SBO219; Accession DDBJ/EMBL/GenBank = AF179839		
<400>	362		
Val Ala Ile Cys His Pro Leu Gln Tyr Ser Val Ile Met Thr Thr Gly			
1	5	10	15
Tyr Cys Gly Gln Leu Val Ala Phe Ser Tyr Met Ser Gly Phe Met Ile			
20	25	30	
Ser Val Ile Lys Val Tyr Phe Ile Ser His Val Ala Phe Cys Gly Ser			
35	40	45	
Asn Val Met Asn Leu Phe Phe Cys Asp Ile Ser Pro Val Leu Lys Leu			
50	55	60	

Ala Cys Lys Asp Met Ser Thr Ala Glu Leu Val Asp Phe Ala Leu Ala
65 70 75 80

Ile Val Ile Leu Val Ile Pro Leu Ile Thr Thr Ile Leu Ser Tyr Ile
85 90 95

Tyr Ile Val Ser Ala Ile Leu His Ile Pro Ser Thr Gln Gly Arg Lys
100 105 110

Lys Ala Phe Ser Thr Cys Ala Ser His Leu Thr Val Val Ile Ile Phe
115 120 125

Tyr Thr Ala Met Ile Phe Thr Tyr Val Arg Pro Arg Ala Ile Ala Ser
130 135 140

Phe Asn Ser Asn Lys Leu Ile Ser Ala Val Tyr Ala Val Leu Thr Pro
145 150 155 160

Met Leu

<210> 363
<211> 488
<212> DNA
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(488)
<223> Taxon = 27679; gene = SBO220; pseudogene; Accession DDBJ/EMBL/GenBank
= AF179840

<400> 363
tgtggccatc tgtaagcccc tgcattacac caccatcatg agcagcaaaa tctgcctgca 60
gcttgtgctt ggggtgctggg ttcttggttt tctcatcatc tttccaccac tctcttagg 120
actaaatcctt gacttctgtg cctccaacgt cggtgatcat ttctactgtg acactatccc 180
gctcctgcag atttctctgca cagacacgca gctcctggag aggatgggat tcatctcagc 240
gctggtgaca ctcttagtca cattggtaat ggtgataata tcatatactt atattgcctt 300
gacaattcta aaaatccctt caactagtca gaggaaaaag gctttttcca cgtgttcttc 360
tcacatgatt gtgatatccc tttcttatgg cagctgccat cttcatgtat gttaagccat 420
cagtcaaaca aagggtatct ttttcaaagg gaatttcggt gctcaatacc tctgttgctc 480
cacttttg 488

<210> 364
<211> 487
<212> DNA
<213> Saimiri boliviensis

<220>

<221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO221; Accession DDBJ/EMBL/GenBank = AF179841

<220>
 <221> CDS
 <222> (2)..(487)
 <223> Product = olfactory receptor

<400> 364
 c gtg gcc atc tgc ctc ccc cta cat tac gcc acc atc atg agc ccc atg 49
 Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
 1 5 10 15
 ctg tct cgc tcc ctg gtg gcg ctg tcc tgg gtg ctg acc acc ttc cat 97
 Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
 20 25 30
 gcc atg ttg cac act tta ctc ata gcc agg ttg cgt ttt tgt gca gac 145
 Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
 35 40 45
 aat gtg atc ttc cac ttt ttc tgt gat atg tct gct ctg ctg aag ctg 193
 Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
 50 55 60
 gcc tgc tct gac act cga gtt aat gaa ttg gtg ata ttt atc atg gga 241
 Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
 65 70 75 80
 ggc ctc att ctt gtc atc cca ttt cta ctt atc att ggg tcc tac gca 289
 Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
 85 90 95
 cga att gtc ttc tcc atc ctc aag gtc cct tct tct aag ggt atc tgc 337
 Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
 100 105 110
 aag gcc gtc tct act tgt ggc tcc cac ctc tct gtg gtg tca ctg ttc 385
 Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
 115 120 125
 tat ggg act gtt att ggt ctc tac tta tgc cca tca gct aat aat tct 433
 Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
 130 135 140
 act cta aag gag act gtc atg gct gtg atg tac act gtg atg gcc ccc 481
 Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
 145 150 155 160
 atg ctg 487
 Met Leu

<210> 365
 <211> 162
 <212> PRT
 <213> Saimiri boliviensis
 <220>
 <221> misc_feature
 <222> (1)..(487)
 <223> Taxon = 27679; gene = SBO221; Accession DDBJ/EMBL/GenBank = AF179841
 <400> 365

Val Ala Ile Cys Leu Pro Leu His Tyr Ala Thr Ile Met Ser Pro Met
1 5 10 15

Leu Ser Arg Ser Leu Val Ala Leu Ser Trp Val Leu Thr Thr Phe His
20 25 30

Ala Met Leu His Thr Leu Leu Ile Ala Arg Leu Arg Phe Cys Ala Asp
35 40 45

Asn Val Ile Phe His Phe Phe Cys Asp Met Ser Ala Leu Leu Lys Leu
50 55 60

Ala Cys Ser Asp Thr Arg Val Asn Glu Leu Val Ile Phe Ile Met Gly
65 70 75 80

Gly Leu Ile Leu Val Ile Pro Phe Leu Leu Ile Ile Gly Ser Tyr Ala
85 90 95

Arg Ile Val Phe Ser Ile Leu Lys Val Pro Ser Ser Lys Gly Ile Cys
100 105 110

Lys Ala Val Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe
115 120 125

Tyr Gly Thr Val Ile Gly Leu Tyr Leu Cys Pro Ser Ala Asn Asn Ser
130 135 140

Thr Leu Lys Glu Thr Val Met Ala Val Met Tyr Thr Val Met Ala Pro
145 150 155 160

Met Leu

<210> 366

<211> 487

<212> DNA

<213> Saimiri boliviensis

<220>

<221> misc_feature

<222> (1)..(487)

<223> Taxon = 27679; gene = SBO222; Accession DDBJ/EMBL/GenBank = AF179842

<220>

<221> CDS

<222> (2)..(487)

<223> Product = olfactory receptor

<400> 366

c gtg gcc atc tgt aac cca ctg ctg tac atg gtc acc atg tct ccc cag 49
Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1 5 10 15

gtg tgt ttg ctc ctt ttg ttg ggt gtc tat ggg atg ggg gtt ttg ggg 97

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Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
      20                      25                      30

gct gtg gct cat aca gga aat ata gtg ttt cta acc ttt tgt gca ggc      145
Ala Val Ala His Thr Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Gly
      35                      40                      45

aac ctt gtc aat cac tac atg tgt gac atc ctt ccc ctt ctt gag ctc      193
Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
      50                      55                      60

tcc tgc aat ggc tct tac ata aat gtt ctg gtc atc ttt att gtt gtg      241
Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val
      65                      70                      75                      80

acc att ggc att ggg gtg ccc att gtt gcc att ttt atc tct tat ggt      289
Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly
      85                      90                      95

ttt att ctt tcc agc aat ctc cac att agt tct gct gag ggc agg tct      337
Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser
      100                      105                      110

aaa gcc ttc agt acc tgc agc tcc cac ata att gca gtt tct ctt ttc      385
Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe
      115                      120                      125

ttc ggg tca gga gct ttt atg tac ctc aaa ccc tct tcc gtt tta ccc      433
Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro
      130                      135                      140

ctg gac cag ggg aaa gta tcc tcc ctg ttt tat act att gtg gtg ccc      481
Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro
      145                      150                      155                      160

atg ttt
Met Phe
      487

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<210> 367
<211> 162
<212> PRT
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO222; Accession DDBJ/EMBL/GenBank = AF179842

<400> 367

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Val Ala Ile Cys Asn Pro Leu Leu Tyr Met Val Thr Met Ser Pro Gln
1                      5                      10                      15

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Val Cys Leu Leu Leu Leu Leu Gly Val Tyr Gly Met Gly Val Leu Gly
      20                      25                      30

```

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Ala Val Ala His Thr Gly Asn Ile Val Phe Leu Thr Phe Cys Ala Gly
      35                      40                      45

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Asn Leu Val Asn His Tyr Met Cys Asp Ile Leu Pro Leu Leu Glu Leu
      50                      55                      60

```

Ser Cys Asn Gly Ser Tyr Ile Asn Val Leu Val Ile Phe Ile Val Val
65 70 75 80

Thr Ile Gly Ile Gly Val Pro Ile Val Ala Ile Phe Ile Ser Tyr Gly
85 90 95

Phe Ile Leu Ser Ser Asn Leu His Ile Ser Ser Ala Glu Gly Arg Ser
100 105 110

Lys Ala Phe Ser Thr Cys Ser Ser His Ile Ile Ala Val Ser Leu Phe
115 120 125

Phe Gly Ser Gly Ala Phe Met Tyr Leu Lys Pro Ser Ser Val Leu Pro
130 135 140

Leu Asp Gln Gly Lys Val Ser Ser Leu Phe Tyr Thr Ile Val Val Pro
145 150 155 160

Met Phe

<210> 368
<211> 487
<212> DNA
<213> Saimiri boliviensis

<220>
<221> misc_feature
<222> (1)..(487)
<223> Taxon = 27679; gene = SBO223; Accession DDBJ/EMBL/GenBank = AF179843

<220>
<221> CDS
<222> (2)..(487)
<223> Product = olfactory receptor

<400> 368
t gtg gcc atc tgt cac ccc ctg cac tac aca gtc acc att aac ccc aga 49
Val Ala Ile Cys His Pro Leu His Tyr Thr Val Thr Ile Asn Pro Arg
1 5 10 15

ctg tgt gga ctg ctg gtt ctg gca tcc tgg atc ctg agt gcc ctg aat 97
Leu Cys Gly Leu Leu Val Leu Ala Ser Trp Ile Leu Ser Ala Leu Asn
20 25 30

tcc tca tta caa acc tta ata gtg ctg cgg ctt tcc ttc tgc aca gac 145
Ser Ser Leu Gln Thr Leu Ile Val Leu Arg Leu Ser Phe Cys Thr Asp
35 40 45

ttg gaa atc ccc cac ttt ttc tgc gaa ctt aat cag gtc ata cat ctt 193
Leu Glu Ile Pro His Phe Phe Cys Glu Leu Asn Gln Val Ile His Leu
50 55 60

gcc tgt tat gac act ttc ctt aat gat gtg gtg atg tat ttg gca gct 241
Ala Cys Tyr Asp Thr Phe Leu Asn Asp Val Val Met Tyr Leu Ala Ala
65 70 75 80

115

120

125

Tyr Gly Thr Leu Leu Gly Val Tyr Leu Ser Ser Ala Ala Thr Gly Asn
 130 135 140

Ser His Ser Ser Ala Ala Ala Leu Val Met Tyr Thr Val Val Thr Pro
 145 150 155 160

Met Leu

<210> 370

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank = AF073959

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 370

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c ata gct gac atc ggc ttc acc tcc acc act atc ccc aag gtt ctg cag      49
  ile ala asp ile gly phe thr ser thr thr ile pro lys val leu gln
   1             5             10             15

act atc cac aca cag agc aaa ttc atc tct ttc tgc ggc tgc atc aca      97
thr ile his thr gln ser lys phe ile ser phe ser gly cys ile thr
      20             25             30

cag ata ttt ttc ttc att gtg ttt gga tgc ctg gac aat tta ctc cta      145
glu ile phe phe phe ile val phe gly cys leu asp asn leu leu leu
      35             40             45

tca gtg atg gcc tat gac cgc ttt gtg gcc atc tgc cat ccc ttg cac      193
ser val met ala tyr asp arg phe val ala ile cys his pro leu his
      50             55             60

tat gtg gtc atc atg aat tct tgc ttc tgt gtg atg ctg gct ctt gga      241
tyr val val ile met asn ser cys phe cys val met leu ala leu gly
      65             70             75             80

tca tgg ata gtc agc gtc atg agt tcc cta cct gag acc ttg act gtg      289
ser trp ile val ser val met ser ser leu pro glu thr leu thr val
      85             90             95

tta aga cta tcc ttc tgt aca aac atg gaa att cca cac ttt ttc tgt      337
leu arg leu ser phe cys thr asn met glu ile pro his phe phe cys
      100            105            110

gat ctt ccc gaa gtc ctg aag ctt gcc tgt tct gac acc ctt gtt aat      385
asp leu pro glu val leu lys leu ala cys ser asp thr leu val asn
      115            120            125

aac att gtg aca tat tct ata acc ata gtc ata gct ggt ttc cca ttc      433

```

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe
 130 135 140
 tct ggg att cta ttg tct tat tct aag att ttc tcc tcc atc cta aga 481
 Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg
 145 150 155 160
 att cct tca gct ggg ggc aag tac aaa gcc ttt tct acc tgt ggg tct 529
 Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cat ctt ttg gtg gtc ttc tta ttc tat agc aat ggt ctt ggg gtc tac 577
 His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr
 180 185 190
 ctc agc tct gca gcc aca tca tct tct aga atg agt cta gtt gcc tca 625
 Leu Ser Ser Ala Ala Thr Ser Ser Arg Met Ser Leu Val Ala Ser
 195 200 205
 ctg atg tac agc ata gtc act ccc 649
 Leu Met Tyr Ser Ile Val Thr Pro
 210 215

<210> 371
 <211> 216
 <212> PRT
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR1-72M15; Accession DDBJ/EMBL/GenBank =
 AF073959

<400> 371
 Ile Ala Asp Ile Gly Phe Thr Ser Thr Thr Ile Pro Lys Val Leu Gln
 1 5 10 15
 Thr Ile His Thr Gln Ser Lys Phe Ile Ser Phe Ser Gly Cys Ile Thr
 20 25 30
 Gln Ile Phe Phe Phe Ile Val Phe Gly Cys Leu Asp Asn Leu Leu Leu
 35 40 45
 Ser Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Val Val Ile Met Asn Ser Cys Phe Cys Val Met Leu Ala Leu Gly
 65 70 75 80
 Ser Trp Ile Val Ser Val Met Ser Ser Leu Pro Glu Thr Leu Thr Val
 85 90 95
 Leu Arg Leu Ser Phe Cys Thr Asn Met Glu Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Pro Glu Val Leu Lys Leu Ala Cys Ser Asp Thr Leu Val Asn

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115              120              125

Asn Ile Val Thr Tyr Ser Ile Thr Ile Val Ile Ala Gly Phe Pro Phe
130              135              140

Ser Gly Ile Leu Leu Ser Tyr Ser Lys Ile Phe Ser Ser Ile Leu Arg
145              150              155              160

Ile Pro Ser Ala Gly Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
165              170              175

His Leu Leu Val Val Phe Leu Phe Tyr Ser Asn Gly Leu Gly Val Tyr
180              185              190

Leu Ser Ser Ala Ala Thr Ser Ser Ser Arg Met Ser Leu Val Ala Ser
195              200              205

Leu Met Tyr Ser Ile Val Thr Pro
210              215

<210> 372
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR1-72M16; Accession DDBJ/EMBL/GenBank =
AF073960

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 372
c ttc tct gac ttc tgc ttt tcc tct gtg acc att ccc aaa ttg ctg cag      49
  Phe Ser Asp Phe Cys Phe Ser Ser Val Thr Ile Pro Lys Leu Leu Gln
   1              5              10              15

aac atg caa agc caa gtt cca tcc ata ccc tat gca ggt tgc ctg gca      97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
   20              25              30

caa atg tac ttt ttc ctg ctt ttt gca gat ctc gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Leu Phe Ala Asp Leu Glu Ser Phe Leu Leu
   35              40              45

gtg gcc atg gcc tat gat cgc tat gtg gcc atc tgc ttc ccc cta cac      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
   50              55              60

tat act agc atc atg agc ccc aag ctg tgt ctc tgc ctg gtg gca cta      241
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Leu Cys Leu Val Ala Leu
   65              70              75              80

tct tgg cta ctg acc aca gtc atc tct ttg tca cac aca ctg ctc atg      289

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      35              40              45
gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat    193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50              55              60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg    241
Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
      65              70              75

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg    289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
      85              90              95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt    337
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
      100             105             110

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat    385
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
      115             120             125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt    433
Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
      130             135             140

gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag    481
Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
      145             150             155

gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc    529
Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
      165             170             175

cac ctg tct gtg gtg tca ctg ttc tat ggg gca atc att ggt ctg tac    577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr
      180             185             190

tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc    625
Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
      195             200             205

atg atg tac aca gtg gtg act ccc                                649
Met Met Tyr Thr Val Val Thr Pro
      210             215

<210> 375
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR10M; Accession DDBJ/EMBL/GenBank = AF073961

<400> 375

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1              5              10              15

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
20             25             30

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Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
 115 120 125

Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ala Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 376

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

<400> 376

t ttc tct gac ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag	49
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln	
1 5 10 15	
aat atg cag agc cag gac cca tcc atc ccc tat gga ggt tgc ctg gca	97
Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala	
20 25 30	
caa ata ttc ttc ttt atg ctt ttt gga gac atg gaa agc ttc ctt ctt	145
Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu	
35 40 45	
gta gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat	193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His	
50 55 60	
tac act agc atc atg agt cct aag gtc tgt act ttt cta gtg cta ctg	241
Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu	
65 70 75 80	
ttg tgg ata ctg aca aca cca cat gcc aca atg caa att ctg ctc aca	289
Leu Trp Ile Leu Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr	
85 90 95	
gta aga ctg tct ttt tgt gag aac aat gtg ttt ctc aac ttt ttc tgt	337
Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys	
100 105 110	
gac ata ttt gtt ctc tta aag ctg gcc tgc tca gac act tat gtt aat	385
Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn	
115 120 125	
gat ttg atg ata ctt atc atg gga ggg ctc atc att gtt att cca ttc	433
Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe	
130 135 140	
ctg ctc att gtt ata tcc tat gca agg atc atc tcc tct act ctt aag	481
Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys	
145 150 155 160	
gtt cca tct act caa ggc atc cac aag gtc ttc tct acc tgt ggc tct	529
Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser	
165 170 175	
cat ctg tct gtg gtg tct ctg ttc tat ggg aca att att ggt ctc tac	577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr	
180 185 190	
tta tgt cca tca ggt aat aat ttc agt cta aag ggg tct gcc atg gct	625
Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala	
195 200 205	
atg atg tac aca gtg gtg act ccc	649
Met Met Tyr Thr Val Val Thr Pro	
210 215	
<210> 377	
<211> 216	
<212> PRT	
<213> Mus musculus domesticus	
<220>	
<221> misc_feature	
<222> (1)..(649)	
<223> Taxon = 10092; clone = OR11M; Accession DDBJ/EMBL/GenBank = AF073962	

<400> 377

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Gly Gly Cys Leu Ala
20 25 30

Gln Ile Phe Phe Phe Met Leu Phe Gly Asp Met Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Val Cys Thr Phe Leu Val Leu Leu
65 70 75 80

Leu Trp Ile Leu Thr Thr Pro His Ala Thr Met Gln Ile Leu Leu Thr
85 90 95

Val Arg Leu Ser Phe Cys Glu Asn Asn Val Phe Leu Asn Phe Phe Cys
100 105 110

Asp Ile Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
115 120 125

Asp Leu Met Ile Leu Ile Met Gly Gly Leu Ile Ile Val Ile Pro Phe
130 135 140

Leu Leu Ile Val Ile Ser Tyr Ala Arg Ile Ile Ser Ser Thr Leu Lys
145 150 155 160

Val Pro Ser Thr Gln Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Gly Asn Asn Phe Ser Leu Lys Gly Ser Ala Met Ala
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 378

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature


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<210>      379
<211>      216
<212>      PRT
<213>      Mus musculus domesticus

<220>
<221>      misc_feature
<222>      (1)..(649)
<223>      Taxon = 10092; clone = OR12M; Accession DDBJ/EMBL/GenBank = AF073963

<400>      379

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1          5          10          15

Asn Met Gln Ser Gln Asp Thr Ser Ile Ser Tyr Ala Gly Cys Leu Thr
          20          25          30

Gln Met Tyr Phe Leu Leu Val Phe Gly Asp Leu Glu Ser Ile Leu Leu
          35          40          45

Leu Val Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Phe Pro Leu His
          50          55          60

Tyr Met Ser Ile Met Ser Pro Thr Leu Cys Val Cys Leu Leu Val Leu
65          70          75          80

Ser Trp Val Phe Thr Val Leu Tyr Ser Met Leu His Thr Leu Leu Leu
          85          90          95

Ser Arg Leu Ser Phe Cys Glu Asp Asn Leu Ile His His Phe Phe Cys
          100          105          110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
          115          120          125

Glu Leu Met Ile Phe Ile Met Gly Gly Leu Val Ser Ile Ile Pro Phe
          130          135          140

Leu Leu Ile Val Val Ser Tyr Ile Gln Ile Val Tyr Ser Ile Leu Lys
145          150          155          160

Ile Ser Ser Ala His Val Leu His Lys Ile Phe Ser Thr Cys Gly Ser
          165          170          175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Phe Ala Leu Tyr
          180          185          190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Ile Ser Met Ala
          195          200          205

Met Met Cys Thr Val Val Thr Pro

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210

215

<210> 380
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank = AF073964

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 380
 c ttt tct gac att ggt ttc atc tct aca act atc cct aag atg ttg gtg 49
 Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
 1 5 10 15
 aat atc caa aca cag agc aag tcc atc tcc tat gca gaa tgc atc acc 97
 Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
 20 25 30
 cag att tat ttt ttc atg ctc ttt gga ggc atg gac ata ctt ctc ctc 145
 Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu Leu
 35 40 45
 acc gtg atg gcc tat gac cga ttt gtg gcc atc tgt cac ccc ctt cac 193
 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 tat tca gtc att atg aat ccc caa cta agt ggc ttg ctg gtt ctt gta 241
 Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
 65 70 75 80
 tca tgg ttt att agc ttt tca tat tct ctg ata cag agt cta ttg atg 289
 Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
 85 90 95
 ctg cgg ttg tcc ttc tgt aca aat cag ata att aaa cac ttt tac tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
 100 105 110
 gaa tat tct aga gcc ctc act ata gcc tgc tca gac aca cta atc aat 385
 Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
 115 120 125
 cat atc ctt ctt tat att ctg ata tgt gtc ctt ggc ttc atc cct ttc 433
 His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
 130 135 140
 tca ggg atc ctt tat tca tac tgt aaa att gtt tct tct att ttg aga 481
 Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
 145 150 155 160
 att cca tca aca gat gga aaa tat aaa gca ttt tct acc tgt ggg tct 529
 Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175
 cat cta tca gtg gtt tct tta ttc tat ggg aca ggc ctt ggt gtg tac 577

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
180 185 190

ctt agt tct gat gta act tcc tcc tct ggg aag gac gtg gtg gcc tca 625
Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser
195 200 205

gta atg tat aca gtg gtc acc cct 649
Val Met Tyr Thr Val Val Thr Pro
210 215

<210> 381
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR15-71M19; Accession DDBJ/EMBL/GenBank =
AF073964

<400> 381

Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Ile Pro Lys Met Leu Val
1 5 10 15

Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr Ala Glu Cys Ile Thr
20 25 30

Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met Asp Ile Leu Leu Leu
35 40 45

Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
50 55 60

Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly Leu Leu Val Leu Val
65 70 75 80

Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile Gln Ser Leu Leu Met
85 90 95

Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile Lys His Phe Tyr Cys
100 105 110

Glu Tyr Ser Arg Ala Leu Thr Ile Ala Cys Ser Asp Thr Leu Ile Asn
115 120 125

His Ile Leu Leu Tyr Ile Leu Ile Cys Val Leu Gly Phe Ile Pro Phe
130 135 140

Ser Gly Ile Leu Tyr Ser Tyr Cys Lys Ile Val Ser Ser Ile Leu Arg
145 150 155 160

Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr Cys Gly Ser

165

170

175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu Gly Val Tyr
 180 185 190

Leu Ser Ser Asp Val Thr Ser Ser Ser Gly Lys Asp Val Val Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 382

<211> 643

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(643)

<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank = AF073965

<220>

<221> CDS

<222> (2)..(643)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 382

g ttc gta gat ctc tgc ttc tca tcc gtc acg gta ccg aaa ctg ctg aag 49
 Phe Val Asp Leu Cys Phe Ser Ser Val Thr Val Pro Lys Leu Leu Lys
 1 5 10 15

gac ctc cta tcg gcg aag aaa acc atc tca ata gaa ggc tgc ctg gct 97
 Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala
 20 25 30

cag gtc ttt ttt gtg ttt ttt cct tct ggt act gaa gcc tgc ctg ctc 145
 Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu
 35 40 45

tct gtc atg gct tat gac cgc tat gct gcc atc tgc cat ccc ctg ctc 193
 Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu
 50 55 60

tac ggc cag gtg atg aga aat gag ttg tgt gta agg ctt gtg gtc atc 241
 Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile
 65 70 75 80

tca tgg ggc gtg gcc tct ctc aac gca acc atc atc gtg ctc ttg gct 289
 Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala
 85 90 95

gtc aac ctg gac ttc tgt ggg gct caa acc att cac cac tac acc tgt 337
 Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys
 100 105 110

gag ctg cct gcc ctt ttc ccc ttg tcc tgt tcc gat atc tcc atc act 385
 Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr
 115 120 125

gtc gtc gtc ctg ctt tgc tcc agc ttg ctg cat ggg ctg gga acc ttt 433

Val Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe
130 135 140

atc cct atc ttc ttc tcc tat gcc cgc att gtc tcc gcc atc ttg agc 481
Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser
145 150 155 160

atc agt tcc acc acc ggg agg agc aag gcc ttc tcc acc tgc tct tcc 529
Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
165 170 175

cac ctc gct gca gtg acc ttg ttc ttt ggg tct ggc ttt ctt tgc tat 577
His Leu Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr
180 185 190

ctc atg ccg cct tct ggt tct tct ctg gac ttg ctc ttg tcg ttg cag 625
Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Ser Leu Gln
195 200 205

tac agc gca gtc acg ccc 643
Tyr Ser Ala Val Thr Pro
210

<210> 383
<211> 214
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 10092; clone = OR15-71M20; Accession DDBJ/EMBL/GenBank =
AF073965

<400> 383

Phe Val Asp Leu Cys Phe Ser Ser Val Thr Val Pro Lys Leu Leu Lys
1 5 10 15

Asp Leu Leu Ser Ala Lys Lys Thr Ile Ser Ile Glu Gly Cys Leu Ala
20 25 30

Gln Val Phe Phe Val Phe Phe Pro Ser Gly Thr Glu Ala Cys Leu Leu
35 40 45

Ser Val Met Ala Tyr Asp Arg Tyr Ala Ala Ile Cys His Pro Leu Leu
50 55 60

Tyr Gly Gln Val Met Arg Asn Glu Leu Cys Val Arg Leu Val Val Ile
65 70 75 80

Ser Trp Gly Val Ala Ser Leu Asn Ala Thr Ile Ile Val Leu Leu Ala
85 90 95

Val Asn Leu Asp Phe Cys Gly Ala Gln Thr Ile His His Tyr Thr Cys
100 105 110

Glu Leu Pro Ala Leu Phe Pro Leu Ser Cys Ser Asp Ile Ser Ile Thr

005030 "G9T" 24260

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115              120              125

Val Val Val Leu Leu Cys Ser Ser Leu Leu His Gly Leu Gly Thr Phe
130              135              140

Ile Pro Ile Phe Phe Ser Tyr Ala Arg Ile Val Ser Ala Ile Leu Ser
145              150              155              160

Ile Ser Ser Thr Thr Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
165              170              175

His Leu Ala Ala Val Thr Leu Phe Phe Gly Ser Gly Phe Leu Cys Tyr
180              185              190

Leu Met Pro Pro Ser Gly Ser Ser Leu Asp Leu Leu Leu Ser Leu Gln
195              200              205

Tyr Ser Ala Val Thr Pro
210

<210> 384
<211> 643
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =
AF073966

<220>
<221> CDS
<222> (2)..(643)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 384
c ctt gtt gac atc ttc ttc tcc tct gta act att ccc aag atg ctg gcc      49
  Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
   1              5              10              15

aac cat ctc cta ggt agc aag gcc atc tcc ttt ggg gga tgt atg gca      97
Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
   20              25              30

cag atg tac ttc atg ata tca ttg gga aac aca gac agt tat ata cta      145
Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
   35              40              45

gct gca atg gca tat gac cga gct gtg gct atc agt cgc ccg ctt cat      193
Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
   50              55              60

tat gca aca att atg agt cca caa ctt tgt gtc ctg ctg gtt gct ggg      241
Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly
   65              70              75              80

tcc tgg gtg att gca aat gct aat gca ctg ccc cac acc cta ctc aca      289
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Ser Trp Val Ile Ala Asn Ala Asn Ala Leu Pro His Thr Leu Leu Thr
      85                      90                      95

gct aga ttg tcc ttc tgt ggc aat aag gat gtg gcc aac ttc tac tgt    337
Ala Arg Leu Ser Phe Cys Gly Asn Lys Asp Val Ala Asn Phe Tyr Cys
      100                      105                      110

gac att aca cct ttg ctc cag ctg tcc tgt tct gac atc cgc ttc aat    385
Asp Ile Thr Pro Leu Leu Gln Leu Ser Cys Ser Asp Ile Arg Phe Asn
      115                      120                      125

gtg aag atg atg tac ctt ggg gtg ggg gtc ttc tct gtg cca ctg ctg    433
Val Lys Met Met Tyr Leu Gly Val Gly Val Phe Ser Val Pro Leu Leu
      130                      135                      140

tgc atc atc atc tcc tat gtc cgg gtc ttt tcc aca gtc ttg cgg gtt    481
Cys Ile Ile Ile Ser Tyr Val Arg Val Phe Ser Thr Val Leu Arg Val
      145                      150                      155                      160

cca tct acc aag ggc ttc ctg aag gcc ttg tcc acc tgt ggc tct cac    529
Pro Ser Thr Lys Gly Phe Leu Lys Ala Leu Ser Thr Cys Gly Ser His
      165                      170                      175

ctg aca gtg gtg tcc ttg tat tat ggg aca gtc atg ggc atg tat ttc    577
Leu Thr Val Val Ser Leu Tyr Tyr Gly Thr Val Met Gly Met Tyr Phe
      180                      185                      190

cgg ccc ctg acc agt tac agt ctg aag cat gca ttg ata act gtg atg    625
Arg Pro Leu Thr Ser Tyr Ser Leu Lys His Ala Leu Ile Thr Val Met
      195                      200                      205

tac acg gca gtg acc cca
Tyr Thr Ala Val Thr Pro
      210

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<210> 385
<211> 214
<212> PRT
<213> Mus musculus domesticus

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<220>
<221> misc_feature
<222> (1)..(643)
<223> Taxon = 10092; clone = OR15-71M21; Accession DDBJ/EMBL/GenBank =
AF073966

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<400> 385

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Leu Val Asp Ile Phe Phe Ser Ser Val Thr Ile Pro Lys Met Leu Ala
1                      5                      10                      15

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Asn His Leu Leu Gly Ser Lys Ala Ile Ser Phe Gly Gly Cys Met Ala
20                      25                      30

```

```

Gln Met Tyr Phe Met Ile Ser Leu Gly Asn Thr Asp Ser Tyr Ile Leu
35                      40                      45

```

```

Ala Ala Met Ala Tyr Asp Arg Ala Val Ala Ile Ser Arg Pro Leu His
50                      55                      60

```

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Tyr Ala Thr Ile Met Ser Pro Gln Leu Cys Val Leu Leu Val Ala Gly

```

[illegible]

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<210> 386
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank =
AF073967

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 386
c ctg gtg gac atc tgc ttt acc act gtc atc gtg cca cag atg tta gtg 49
  Leu Val Asp Ile Cys Phe Thr Thr Val Ile Val Pro Gln Met Leu Val
   1             5             10             15

aac ttg ctg aca cag aga aag aca atc ctc ttt gcc cag tgc ctc act 97
Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr
   20             25             30

caa atg tat ttc ttt gtg gct ttt ggt att aca gac agt ttc ctt ttg 145

```

Gln	Met	Tyr	Phe	Phe	Val	Ala	Phe	Gly	Ile	Thr	Asp	Ser	Phe	Leu	Leu		
	35						40					45					
gct	gcg	atg	gcc	att	gac	cgc	tat	gtt	gct	att	tgc	aat	ccg	ctt	cat	193	
Ala	Ala	Met	Ala	Ile	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Asn	Pro	Leu	His		
	50					55					60						
tac	aac	aca	gtc	atg	agt	ccc	agg	cgc	tgt	cgc	ttg	ctg	ggt	gtg	gca	241	
Tyr	Asn	Thr	Val	Met	Ser	Pro	Arg	Arg	Cys	Arg	Leu	Leu	Val	Val	Ala		
65					70					75					80		
tcc	tgg	gca	gtg	tcc	cat	ctt	cac	tcc	ctc	acc	cac	aca	att	ctc	atg	289	
Ser	Trp	Ala	Val	Ser	His	Leu	His	Ser	Leu	Thr	His	Thr	Ile	Leu	Met		
				85					90					95			
ggc	cgc	ctc	tct	ttc	tgt	gga	ccc	aat	gtc	att	cat	cac	ttc	ttt	tgt	337	
Gly	Arg	Leu	Ser	Phe	Cys	Gly	Pro	Asn	Val	Ile	His	His	Phe	Phe	Cys		
			100					105					110				
gat	gtc	cag	cca	ctg	ctg	aca	ctc	tcc	tgc	tct	gac	acc	tct	atc	aat	385	
Asp	Val	Gln	Pro	Leu	Leu	Thr	Leu	Ser	Cys	Ser	Asp	Thr	Ser	Ile	Asn		
		115					120					125					
gag	ctc	ttg	gcc	ttc	aca	gag	ggc	tct	gtt	gta	atc	atg	agc	cct	ttt	433	
Glu	Leu	Leu	Ala	Phe	Thr	Glu	Gly	Ser	Val	Val	Ile	Met	Ser	Pro	Phe		
	130					135					140						
atc	tta	ttg	ttg	tct	ctt	ata	tct	ata	ttc	act	cgg	act	gtt	ctg	agg	481	
Ile	Leu	Leu	Leu	Ser	Leu	Ile	Ser	Ile	Phe	Thr	Arg	Thr	Val	Leu	Arg		
145					150					155					160		
gtc	cct	tca	ggg	gaa	gga	agg	tac	aaa	gtt	ttc	tct	acc	tgt	ggg	tct	529	
Val	Pro	Ser	Gly	Glu	Gly	Arg	Tyr	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser		
				165					170					175			
cac	ctc	aca	gtt	gta	gca	ctg	ttc	tat	gga	acc	ata	ata	tca	gtg	tac	577	
His	Leu	Thr	Val	Val	Ala	Leu	Phe	Tyr	Gly	Thr	Ile	Ile	Ser	Val	Tyr		
			180					185					190				
att	cgc	ccc	tca	tcc	acc	tac	tca	gtg	aca	aag	gac	cga	gtt	gtc	act	625	
Ile	Arg	Pro	Ser	Ser	Thr	Tyr	Ser	Val	Thr	Lys	Asp	Arg	Val	Val	Thr		
		195					200					205					
gtc	atc	tat	aca	gta	gtt	acc	cca									649	
Val	Ile	Tyr	Thr	Val	Val	Thr	Pro										
	210					215											

<210> 387
 <211> 216
 <212> PRT
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR15-71M24; Accession DDBJ/EMBL/GenBank = AF073967
 <400> 387

Leu	Val	Asp	Ile	Cys	Phe	Thr	Thr	Val	Ile	Val	Pro	Gln	Met	Leu	Val
1				5					10					15	

Asn Leu Leu Thr Gln Arg Lys Thr Ile Leu Phe Ala Gln Cys Leu Thr

<400>	388	
c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag		49
Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln		
1 5 10 15		
aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg aca		97
Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr		
20 25 30		
caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt ctt		145
Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu		
35 40 45		
gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt caa		193
Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln		
50 55 60		
tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg ttc		241
Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe		
65 70 75 80		
tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc ttg		289
Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu		
85 90 95		
gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc tgt		337
Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys		
100 105 110		
gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att aat		385
Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn		
115 120 125		
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc		433
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu		
130 135 140		
tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg		481
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg		
145 150 155 160		
att tct tct act cgg gct atc cat aag ctc ttc tcc acc tgt ggc tca		529
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser		
165 170 175		
cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac		577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr		
180 185 190		
tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc		625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser		
195 200 205		
ctg atg tac aca gtg gtg act ccc		649
Leu Met Tyr Thr Val Val Thr Pro		
210 215		
<210>	389	
<211>	216	
<212>	PRT	
<213>	Mus musculus domesticus	
<220>		
<221>	misc feature	

<222> (1)..(649)
 <223> Taxon = 10092; clone = OR18M; Accession DDBJ/EMBL/GenBank = AF073968
 <400> 389

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
 20 25 30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
 35 40 45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
 50 55 60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
 65 70 75 80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
 85 90 95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110

Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
 130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 390
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR1M; Accession DDBJ/EMBL/GenBank = AF073969

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

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<400> 390
c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag      49
  Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
    1             5             10             15

aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca      97
Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
      20             25             30

caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt      145
Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
      35             40             45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50             55             60

tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta      241
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
      65             70             75             80

ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca      289
Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
      85             90             95

gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt      337
Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
      100            105            110

gac cta ttt gtt ctc cta aag ctg gct tgc tca gac act tat gtt aat      385
Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
      115            120            125

gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt      433
Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe
      130            135            140

ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag      481
Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys
      145            150            155            160

gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc      529
Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser
      165            170            175

cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac      577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
      180            185            190

tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc      625
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala
      195            200            205

atg atg tac aca gtg gtg act ccc      649
Met Met Tyr Thr Val Val Thr Pro
  
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Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 392
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR21M; Accession DDBJ/EMBL/GenBank = AF073970
 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

<400> 392
 c ttt gca gac atc tgc ttt act tct gct agc atc cca aag atg cta gtg 49
 Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val
 1 5 10 15
 aat ata cag aca aag aac aag gtg ata acc tat gaa ggt tgc att tct 97
 Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser
 20 25 30
 caa gta ttc ttt ttc ata cta ttt gga gtt tta gat aac ttt ctt cta 145
 Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu
 35 40 45
 gct gtg atg gcc tat gac cga tat gtg gca atc tgt cac cct ctg cac 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
 50 55 60
 tat atg gtc atc atg aac cgc cgc ctc tgt gga ttt tta gtt ttg ggg 241
 Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly
 65 70 75 80
 tct tgg gtc aca aca gca ttg aat tcc ttg ctg cag agt tca atg gca 289
 Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala
 85 90 95
 ctg cgg ctg tcc ttt tgt aca gac ttg aaa att ccc cac ttt gtt tgt 337
 Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys
 100 105 110
 gag ctt aat caa ctg gta cta ctt gcc tgt aat gac acc ttt cct aat 385
 Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn
 115 120 125
 gac atg gtg atg tac ttt gca gct ata ctg ctg ggt ggt ggt cct ctt 433
 Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu
 130 135 140
 gct ggc atc ctt tac tct tat tct aag ata gtt tcc tcc ata cgt gca 481
 Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
 145 150 155 160
 atc tca tca tca cag ggg aag tat aaa gca tcc tcc acc tgt gca tcc 529
 Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser
 165 170 175

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cac ctc tca gtt gtt tca tta ttc tat tct tca ctc ttg ggt gcg tat      577
His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
      180                      185                      190

ctt agt tct tct ttt aca caa aac tca cac tca act gca cga gca tct      625
Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser
      195                      200                      205

gtt atg tac agt gtg gtc acc ccc      649
Val Met Tyr Ser Val Val Thr Pro
      210                      215

<210> 393
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR21M; Accession DDBJ/EMBL/GenBank = AF073970

<400> 393

Phe Ala Asp Ile Cys Phe Thr Ser Ala Ser Ile Pro Lys Met Leu Val
1          5                      10                      15

Asn Ile Gln Thr Lys Asn Lys Val Ile Thr Tyr Glu Gly Cys Ile Ser
      20                      25                      30

Gln Val Phe Phe Phe Ile Leu Phe Gly Val Leu Asp Asn Phe Leu Leu
      35                      40                      45

Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu His
      50                      55                      60

Tyr Met Val Ile Met Asn Arg Arg Leu Cys Gly Phe Leu Val Leu Gly
65          70                      75                      80

Ser Trp Val Thr Thr Ala Leu Asn Ser Leu Leu Gln Ser Ser Met Ala
      85                      90                      95

Leu Arg Leu Ser Phe Cys Thr Asp Leu Lys Ile Pro His Phe Val Cys
      100                      105                      110

Glu Leu Asn Gln Leu Val Leu Leu Ala Cys Asn Asp Thr Phe Pro Asn
      115                      120                      125

Asp Met Val Met Tyr Phe Ala Ala Ile Leu Leu Gly Gly Gly Pro Leu
      130                      135                      140

Ala Gly Ile Leu Tyr Ser Tyr Ser Lys Ile Val Ser Ser Ile Arg Ala
145          150                      155                      160

Ile Ser Ser Ser Gln Gly Lys Tyr Lys Ala Ser Ser Thr Cys Ala Ser

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165                               170                               175

His Leu Ser Val Val Ser Leu Phe Tyr Ser Thr Leu Leu Gly Ala Tyr
180                               185                               190

Leu Ser Ser Ser Phe Thr Gln Asn Ser His Ser Thr Ala Arg Ala Ser
195                               200                               205

Val Met Tyr Ser Val Val Thr Pro
210                               215

<210> 394
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 394
c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag      49
  Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
   1              5              10              15

aac atg cag agc cag gac tca tcc atc acc tat gca gga tgc ctg aca      97
Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
   20              25              30

caa atg tac ttt ttc ttg ctc ttt gga gac ctt gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
   35              40              45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc ccc ctt cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
   50              55              60

tac atg agc atc atg agc ccc agc ctc tgt gtg agt ctg gtg ctg ctg      241
Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
   65              70              75              80

tcc tgg gtg ctg acc act ttc cat gcc atg ctg cat acc ctg ctc atg      289
Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
   85              90              95

gcc aga ttg tca ttc tgt gag gac aat gtg atc ccc tac ttt ttc tgt      337
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
  100              105              110

gac atg tct gct ctg ctg aag ctg tcc tgc tct gac act cac gtt aat      385
Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
  115              120              125

gaa ttg gtg ata ttt gtc aca gga ggc ctg atc ctt gtc att cca ttt      433
Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe

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130          135          140
gtg ctc atc ctt gtg tcc tat gca cga att gtg tcc tcc att ctc aag      481
Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
145          150          155          160

gtc ccg tct gct cga ggc atc cgt aaa gcc ttc tcc acc tgt ggg tcc      529
Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
          165          170          175

cac ctg tct gtg gtg tca ctg ttc tat ggg aca atc att ggt ctg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
          180          185          190

tta tgt cca tca gct gat aac tct act gtg aag gaa act gtc atg gcc      625
Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
          195          200          205

atg atg tac aca gtg gtg act ccc      649
Met Met Tyr Thr Val Val Thr Pro
          210          215

<210> 395
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR22M; Accession DDBJ/EMBL/GenBank = AF073971

<400> 395

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1          5          10          15

Asn Met Gln Ser Gln Asp Ser Ser Ile Thr Tyr Ala Gly Cys Leu Thr
          20          25          30

Gln Met Tyr Phe Phe Leu Leu Phe Gly Asp Leu Glu Ser Phe Leu Leu
          35          40          45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          50          55          60

Tyr Met Ser Ile Met Ser Pro Ser Leu Cys Val Ser Leu Val Leu Leu
65          70          75          80

Ser Trp Val Leu Thr Thr Phe His Ala Met Leu His Thr Leu Leu Met
          85          90          95

Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro Tyr Phe Phe Cys
          100          105          110

Asp Met Ser Ala Leu Leu Lys Leu Ser Cys Ser Asp Thr His Val Asn
          115          120          125

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Glu Leu Val Ile Phe Val Thr Gly Gly Leu Ile Leu Val Ile Pro Phe
 130 135 140

Val Leu Ile Leu Val Ser Tyr Ala Arg Ile Val Ser Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Ala Arg Gly Ile Arg Lys Ala Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asp Asn Ser Thr Val Lys Glu Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Val Val Thr Pro
 210 215

<210> 396
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

<400> 396
 c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49
 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
 1 5 10 15
 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97
 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30
 caa atg tac ttc ttt ttg ttt ttc ggt gat gtt gag agt tta ctc ctt 145
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
 35 40 45
 gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg 241
 Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
 65 70 75 80
 tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta 289
 Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
 85 90 95

```

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt      337
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
      100                      105                      110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat      385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
      115                      120                      125

gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt      433
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
      130                      135                      140

cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa      481
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
      145                      150                      155                      160

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggg tct      529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
      165                      170                      175

cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
      180                      185                      190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct      625
Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
      195                      200                      205

atg atg tac act gtg gtg att ccc      649
Met Met Tyr Thr Val Val Ile Pro
      210                      215

<210> 397
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR25M; Accession DDBJ/EMBL/GenBank = AF073972

<400> 397

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
1      5      10      15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
      20      25      30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
      35      40      45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
      50      55      60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65      70      75      80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu

```

	85		90		95	
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys	100		105		110	
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn	115		120		125	
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe	130		135		140	
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys	145		150		155	160
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser	165		170		175	
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr	180		185		190	
Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser	195		200		205	
Met Met Tyr Thr Val Val Ile Pro	210		215			

<210> 398
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

 <400> 398
 c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa 49
 Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
 1 5 10 15

 aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca 97
 Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

 caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agt tta ctc ctt 145
 Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
 35 40 45

 gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc tcc cct ctt cat 193
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His

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      50              55              60
tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg      241
Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65              70              75              80

tcc tgg gca ctg aca ttg tat gcc atg ttg cac act ttg ctc tta      289
Ser Trp Ala Leu Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85              90              95

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt      337
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100              105              110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat      385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115              120              125

gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt      433
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130              135              140

cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc act ctc aaa      481
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys
145              150              155

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct      529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165              170              175

cat ctg tct gtg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180              185              190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct      625
Leu Cys Pro Ser Ser Asn Asn Thr Val Lys Asp Thr Val Met Ser
195              200              205

atg atg tac act gtg gtg act ccc
Met Met Tyr Thr Val Val Thr Pro
210              215

<210> 399
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR27M; Accession DDBJ/EMBL/GenBank = AF073973

<400> 399

Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
1              5              10              15

Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
20              25              30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
35              40              45

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Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Ser Pro Leu His
50 55 60

Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
65 70 75 80

Ser Trp Ala Leu Thr Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Thr Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
180 185 190

Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
195 200 205

Met Met Tyr Thr Val Val Thr Pro
210 215

<210> 400
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 400
a gtg gtg gac atc tgc tac acc tcc agt ggg gtc ccc cag atg ctg gca 49
Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala
1 5 10 15

cac ttc ctc atg gag aaa aag acc atc tct ttt gcc cta tgt ggg acc His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr 20 25 30	97
cag ctc ttc ttt gct ctg act ctt ggg gga act gag ttt ctg ttg ctg Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu Leu 35 40 45	145
act gcc atg gcc tat gac cgc tat gtg gct gtc tgt aat cca tta cgg Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg 50 55 60	193
tac aca gtg gtg atg aac cca agg ctc tgc atg ggt cta gca ggt gtc Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val 65 70 75 80	241
tct tgg ttt gtg ggt gta gtt aat tct gct gtg gag aca gca gtc acc Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr 85 90 95	289
atg tac ctt ccc acc tgt ggg cac aat gta ctc aac cat gtg gcc tgt Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys 100 105 110	337
gag aca ctg gca ctg gtc aga ctg gcc tgt gtg gac atc acc ctc aac Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn 115 120 125	385
caa gtg gtg ata ctg gct tct agt gtg gtg gtg ctg atg ata ccc tgc Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys 130 135 140	433
tct ctg gtc tct ctg tcc tat gcc cac att gta gct gcc atc atg aag Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys 145 150 155 160	481
atc cgt tct acc cag gga cgc cgc aaa gcc ttt gag acc tgt gcc tcc Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser 165 170 175	529
cat ctg act gtg gtc tcc atg tct tat ggg atg gcc ctc ttc acc tac His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr 180 185 190	577
ctg cag cct gcc tcc aca gcc tct gct gag cag gac aag gtg gta gtg Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val 195 200 205	625
atc ttc tat gct ttg gtc acc ccc Ile Phe Tyr Ala Leu Val Thr Pro 210 215	649

<210> 401
 <211> 216
 <212> PRT
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR28M; Accession DDBJ/EMBL/GenBank = AF073974
 <400> 401

Val Val Asp Ile Cys Tyr Thr Ser Ser Gly Val Pro Gln Met Leu Ala

097433.0000
F06000 "GAT24260"

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1             5             10             15

His Phe Leu Met Glu Lys Lys Thr Ile Ser Phe Ala Leu Cys Gly Thr
    20                      25                      30

Gln Leu Phe Phe Ala Leu Thr Leu Gly Gly Thr Glu Phe Leu Leu Leu
    35                      40                      45

Thr Ala Met Ala Tyr Asp Arg Tyr Val Ala Val Cys Asn Pro Leu Arg
    50                      55                      60

Tyr Thr Val Val Met Asn Pro Arg Leu Cys Met Gly Leu Ala Gly Val
    65                      70                      75                      80

Ser Trp Phe Val Gly Val Val Asn Ser Ala Val Glu Thr Ala Val Thr
    85                      90                      95

Met Tyr Leu Pro Thr Cys Gly His Asn Val Leu Asn His Val Ala Cys
    100                     105                     110

Glu Thr Leu Ala Leu Val Arg Leu Ala Cys Val Asp Ile Thr Leu Asn
    115                     120                     125

Gln Val Val Ile Leu Ala Ser Ser Val Val Val Leu Met Ile Pro Cys
    130                     135                     140

Ser Leu Val Ser Leu Ser Tyr Ala His Ile Val Ala Ala Ile Met Lys
    145                     150                     155                     160

Ile Arg Ser Thr Gln Gly Arg Arg Lys Ala Phe Glu Thr Cys Ala Ser
    165                     170                     175

His Leu Thr Val Val Ser Met Ser Tyr Gly Met Ala Leu Phe Thr Tyr
    180                     185                     190

Leu Gln Pro Ala Ser Thr Ala Ser Ala Glu Gln Asp Lys Val Val Val
    195                     200                     205

Ile Phe Tyr Ala Leu Val Thr Pro
    210                     215

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<210> 402
<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR29M; Accession DDBJ/EMBL/GenBank = AF073975

<220>

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<221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

<400> 402

t ttc gtt gac ctc tgc cag tcc agt gtc atc atg ccc aaa atg ctg gag 49
 Phe Val Asp Leu Cys Gln Ser Ser Val Ile Met Pro Lys Met Leu Glu
 1 5 10 15

aaa ttt gtc atg gtg aag agt gtc att tct ttt gca gaa tgc atg gct 97
 Lys Phe Val Met Val Lys Ser Val Ile Ser Phe Ala Glu Cys Met Ala
 20 25 30

cag ttt tac tta ttt gat gtt ttt gct gtt tca gag tgt cac atg ctg 145
 Gln Phe Tyr Leu Phe Asp Val Phe Ala Val Ser Glu Cys His Met Leu
 35 40 45

gct gtc atg gct tat gat cgc tat gtt gcc atc tgt aac ccc ttg cta 193
 Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Asn Pro Leu Leu
 50 55 60

tat aat gtt acc atg tct tac aaa gtg tgt tcc tgg atg gta gtg ggg 241
 Tyr Asn Val Thr Met Ser Tyr Lys Val Cys Ser Trp Met Val Val Gly
 65 70 75 80

gtg tat agt gta ggc ttg att tgt gcc aca ggg gaa aca gtc tgc ctg 289
 Val Tyr Ser Val Gly Leu Ile Cys Ala Thr Gly Glu Thr Val Cys Leu
 85 90 95

ctt aga ctg cta ttc tgc aaa gct gat gac ata aac cac tac ttc tgt 337
 Leu Arg Leu Leu Phe Cys Lys Ala Asp Asp Ile Asn His Tyr Phe Cys
 100 105 110

gat ctt tta cca cta ctg gaa caa tcc tgt tcc aat aca ttt atc aat 385
 Asp Leu Leu Pro Leu Leu Glu Gln Ser Cys Ser Asn Thr Phe Ile Asn
 115 120 125

gaa ata cta gga ctg tcc ttc agt tca ttt aat act act gtc cca gct 433
 Glu Ile Leu Gly Leu Ser Phe Ser Ser Phe Asn Thr Thr Val Pro Ala
 130 135 140

ctg acc atc ctc agt tcc tac atc ttc atc ata gcc agc atc ctc cgc 481
 Leu Thr Ile Leu Ser Ser Tyr Ile Phe Ile Ile Ala Ser Ile Leu Arg
 145 150 155 160

att cct tcc act gaa ggc agg tcc aaa gcc ttc agc acc tgc agc tcc 529
 Ile Pro Ser Thr Glu Gly Arg Ser Lys Ala Phe Ser Thr Cys Ser Ser
 165 170 175

cac atc ttg gct gtt gct gtc ttc ttt ggg tct tta gca ttc atg tac 577
 His Ile Leu Ala Val Ala Val Phe Phe Gly Ser Leu Ala Phe Met Tyr
 180 185 190

ctt cag cca tca tca gtc agc tcc atg gac caa ggg aaa gtg tcc tct 625
 Leu Gln Pro Ser Ser Val Ser Ser Met Asp Gln Gly Lys Val Ser Ser
 195 200 205

gtg ttt tat acc att gtt gtg ccc 649
 Val Phe Tyr Thr Ile Val Val Pro
 210 215

<210> 403

<211> 216

<212> PRT


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<211> 649
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 404
c ttc act gac ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag      49
  Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
    1             5             10             15

aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca      97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
          20             25             30

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt      145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
          35             40             45

gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          50             55             60

tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg      241
Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
          65             70             75             80

tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta      289
Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
          85             90             95

act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt      337
Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
          100            105            110

gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat      385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
          115            120            125

gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt      433
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
          130            135            140

cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag      481
Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
          145            150            155            160

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct      529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
          165            170            175

cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
          180            185            190

tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser

```

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195                200                205
ctg atg tac act gtg gta act ccc
Leu Met Tyr Thr Val Val Thr Pro
210                215

<210> 405
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR2M; Accession DDBJ/EMBL/GenBank = AF073976

<400> 405

Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1                5                10                15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20                25                30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
35                40                45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50                55                60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
65                70                75                80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
85                90                95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
100                105                110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115                120                125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
130                135                140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
145                150                155                160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165                170                175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180                185                190

```

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 406
 <211> 650
 <212> DNA
 <213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(650)
 <223> Taxon = 10092; clone = OR3M; Accession DDBJ/EMBL/GenBank = AF073977

<220>
 <221> CDS
 <222> (3)..(650)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

<400> 406
 cc ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg 47
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu
 1 5 10 15
 cag aac atg cag atc cag gac aca ccc ata tcc tat gtg gct tgt ctg 95
 Gln Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu
 20 25 30
 aca caa atg tac ttt ttc agt gtt ttt gga agt ctg gag ata ttc ctt 143
 Thr Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu
 35 40 45
 ctt gta gtc ctg gcc tat gac cgc tat gtg gcc atc tgt tta ccc ctt 191
 Leu Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu
 50 55 60
 caa tat tcc agc atc atg agc ccc aat ctc tgt gtg tgt gtg gtg gtg 239
 Gln Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val
 65 70 75
 ttc tgc tgg gta ttt att gtg ttt tat gcc atg ttt cac aca cta ctc 287
 Phe Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu
 80 85 90 95
 ttg gct aga ttg tca ttt tgt aag aac aat gtg atc cca cac ttt ttc 335
 Leu Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe
 100 105 110
 tgt gac ata tct gcc ctt ctg aag ttg gca tgc tct gat gtt tat att 383
 Cys Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile
 115 120 125
 aat gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc acc tca 431
 Asn Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Thr Ser
 130 135 140
 ctc tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta 479
 Leu Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu
 145 150 155


```

115              120              125
gaa tta atg ata ctt atc ttg gga ggg ttt ctt ctt gtc atc tca ctc      433
Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
130              135              140

tta ctc atc att gta tcc tat gta caa att gtc tcc tca att tta agg      481
Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
145              150              155              160

att tct tct act cgg gct atc cat aag ctc ttc tcc acc tgt ggc tca      529
Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
165              170              175

cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt ctg tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180              185              190

tta tgt cca tca gct aat aac tct act gaa aag gag act gcc atg tcc      625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
195              200              205

ctg atg tac aca gtg gtg act cc      648
Leu Met Tyr Thr Val Val Thr
210              215

<210> 409
<211> 215
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(648)
<223> Taxon = 10092; clone = OR4M; Accession DDBJ/EMBL/GenBank = AF073978

<400> 409

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1          5          10          15

Asn Met Gln Ile Gln Asp Thr Pro Ile Ser Tyr Val Ala Cys Leu Thr
20          25          30

Gln Met Tyr Phe Phe Ser Val Phe Gly Ser Leu Glu Ile Phe Leu Leu
35          40          45

Val Val Leu Ala Tyr Asp Arg Tyr Val Ala Ile Cys Leu Pro Leu Gln
50          55          60

Tyr Ser Ser Ile Met Ser Pro Asn Leu Cys Val Cys Val Val Val Phe
65          70          75          80

Cys Trp Val Phe Ile Val Phe Tyr Ala Met Phe His Thr Leu Leu Leu
85          90          95

Ala Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
100          105          110

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Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Val Tyr Ile Asn
 115 120 125

Glu Leu Met Ile Leu Ile Leu Gly Gly Phe Leu Leu Val Ile Ser Leu
 130 135 140

Leu Leu Ile Ile Val Ser Tyr Val Gln Ile Val Ser Ser Ile Leu Arg
 145 150 155 160

Ile Ser Ser Thr Arg Ala Ile His Lys Leu Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Glu Lys Glu Thr Ala Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr
 210 215

<210> 410

<211> 649

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(649)

<223> Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank = AF073979

<220>

<221> CDS

<222> (2)..(649)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 410

c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag 49
 Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
 1 5 10 15

aac atg cag agc cag gac cca tcc atc ccc tat gcc agc tgt ctg aca 97
 Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr
 20 25 30

caa atg tac ttt ttc atg gct ttt ggg aac atg gaa att tat ctt ctt 145
 Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu
 35 40 45

gtg gtc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctt cat 193
 Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

tac acc agc atc atg agc cct aag ctc tgt gtg tct ctg gtg gtt ctc 241
 Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu
 65 70 75 80

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tct tgg gta ttt acc att ctg tat tcc atg tta cac acc cta ctc ttg      289
Ser Trp Val Phe Thr Ile Leu Tyr Ser Met Leu His Thr Leu Leu Leu
                        85                      90                      95

gca aga ttg tca ttc tgt gag gac aat gtg atc ccc cac ttt ttc tgt      337
Ala Arg Leu Ser Phe Cys Glu Asp Asn Val Ile Pro His Phe Phe Cys
                        100                      105                      110

gac ata tct gcc ctg ctc aag ttg gcc tgc tct gac att tct att aat      385
Asp Ile Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile Ser Ile Asn
                        115                      120                      125

gaa cta atg ata ttt atc gtg gga ggg ctt gat act gta atc cca ttt      433
Glu Leu Met Ile Phe Ile Val Gly Gly Leu Asp Thr Val Ile Pro Phe
                        130                      135                      140

tta ctc att gtt gtt tcc tat gta caa att gtc tgc tcc att cta aag      481
Leu Leu Ile Val Val Ser Tyr Val Gln Ile Val Cys Ser Ile Leu Lys
145                      150                      155                      160

ttc tca tct aca cgg ggc ata cac aag gtc ttc tcc acc tgt ggc tcc      529
Phe Ser Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
                        165                      170                      175

cac ctg tct gtg gtc tca ctg ttc tat ggg aca att att ggt gtc tac      577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Val Tyr
                        180                      185                      190

ata tgc cca tca gct aat aac tct act gtg aag gag act gtc atg tcc      625
Ile Cys Pro Ser Ala Asn Asn Ser Thr Val Lys Glu Thr Val Met Ser
                        195                      200                      205

ctg atg tac aca gtg gtg acg ccc      649
Leu Met Tyr Thr Val Val Thr Pro
210                      215

<210> 411
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR5M; Accession DDBJ/EMBL/GenBank = AF073979

<400> 411

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1                      5                      10                      15

Asn Met Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Ser Cys Leu Thr
20                      25                      30

Gln Met Tyr Phe Phe Met Ala Phe Gly Asn Met Glu Ile Tyr Leu Leu
35                      40                      45

Val Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50                      55                      60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Val Ser Leu Val Val Leu

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35					40					45										
gtg	gcc	atg	gcc	tat	gac	cga	tat	gta	gcc	atc	tgc	ttc	cct	ctt	cat	193				
Val	Ala	Met	Ala	Tyr	Asp	Arg	Tyr	Val	Ala	Ile	Cys	Phe	Pro	Leu	His					
50					55					60										
tac	acc	agc	att	atg	agc	ccc	agg	ctc	tgt	gtg	agt	ctt	gtg	ctg	ctg	241				
Tyr	Thr	Ser	Ile	Met	Ser	Pro	Arg	Leu	Cys	Val	Ser	Leu	Val	Leu	Leu					
65					70					75					80					
tcc	tgg	ttg	ctg	acc	atg	tcc	cat	tcc	atg	ctg	cac	act	ttg	ctc	tta	289				
Ser	Trp	Leu	Leu	Thr	Met	Ser	His	Ser	Met	Leu	His	Thr	Leu	Leu	Leu					
85					90					95										
act	agg	ttg	tct	ttc	tgt	gaa	aac	aat	gtg	atc	ccc	cat	ttt	ttc	tgt	337				
Thr	Arg	Leu	Ser	Phe	Cys	Glu	Asn	Asn	Val	Ile	Pro	His	Phe	Phe	Cys					
100					105					110										
gat	ctg	tct	gct	ctg	ctg	aag	ctg	gcc	tgc	tct	gat	att	cac	att	aat	385				
Asp	Leu	Ser	Ala	Leu	Leu	Lys	Leu	Ala	Cys	Ser	Asp	Ile	His	Ile	Asn					
115					120					125										
gaa	ttg	gtg	ata	ttg	atc	ata	gga	ggg	ctt	gtt	gtt	ata	ctt	cca	ttt	433				
Glu	Leu	Val	Ile	Leu	Ile	Ile	Gly	Gly	Leu	Val	Val	Ile	Leu	Pro	Phe					
130					135					140										
cta	ctc	gtc	aca	gtg	cct	tat	gca	cgc	atc	atc	tcc	tcc	att	ctc	aag	481				
Leu	Leu	Val	Thr	Val	Pro	Tyr	Ala	Arg	Ile	Ile	Ser	Ser	Ile	Leu	Lys					
145					150					155					160					
gtc	cct	tca	act	cga	ggc	atc	cac	aag	gtc	ttc	tcc	act	tgt	ggg	tct	529				
Val	Pro	Ser	Thr	Arg	Gly	Ile	His	Lys	Val	Phe	Ser	Thr	Cys	Gly	Ser					
165					170					175										
cac	ctg	tct	gtg	gtg	tca	ctg	ttc	tat	ggg	aca	att	att	ggc	ctc	tac	577				
His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Ile	Ile	Gly	Leu	Tyr					
180					185					190										
tta	tgt	cca	tct	gct	aat	aac	tct	act	cta	aag	gac	act	gtc	atg	tct	625				
Leu	Cys	Pro	Ser	Ala	Asn	Asn	Ser	Thr	Leu	Lys	Asp	Thr	Val	Met	Ser					
195					200					205										
ctg	atg	tac	act	gtg	gta	act	ccc									649				
Leu	Met	Tyr	Thr	Val	Val	Thr	Pro													
210					215															

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<210> 413
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR6M; Accession DDBJ/EMBL/GenBank = AF073980

<400> 413
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Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
1 5 10 15

Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
 35 40 45
 Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60
 Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
 65 70 75 80
 Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
 85 90 95
 Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
 115 120 125
 Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
 130 135 140
 Leu Leu Val Thr Val Pro Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
 145 150 155 160
 Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175
 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190
 Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205
 Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 414
 <211> 649
 <212> DNA
 <213> Mus musculus domesticus

 <220>
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 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981

 <220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

 <400> 414


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c ttc act gac ctc tgc ttt tct act gtc aca atg ccc aat ttc ctg caa      49
  Phe Thr Asp Leu Cys Phe Ser Thr Val Thr Met Pro Asn Phe Leu Gln
    1             5             10             15

aac atg cag agc caa gta tca tcc att ccc tat gca ggc tgc ctt gca      97
Asn Met Gln Ser Gln Val Ser Ser Ile Pro Tyr Ala Gly Cys Leu Ala
          20             25             30

caa atg tac ttc ttt ttg ttt ttt ggt gat gtt gag agc tta ctc ctt      145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Val Glu Ser Leu Leu Leu
          35             40             45

gtt gcc atg gcc tat gac cgt tat gtg gcc atc tgc ttc cct ctt cat      193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          50             55             60

tat acc aga atc atg agc cca aac ctc tgt gtg agt atg gtg ctg ctg      241
Tyr Thr Arg Ile Met Ser Pro Asn Leu Cys Val Ser Met Val Leu Leu
          65             70             75             80

tcc tgg gca ctg aca aca ttg tat gcc atg ttg cac act ttg ctc tta      289
Ser Trp Ala Leu Thr Leu Tyr Ala Met Leu His Thr Leu Leu Leu
          85             90             95

act agg ttg tct ttc tgt aaa aac aat gtg atc ccc cat ttt ttc tgt      337
Thr Arg Leu Ser Phe Cys Lys Asn Asn Val Ile Pro His Phe Phe Cys
          100             105             110

gac ctt tct gct ctc ctg aag ctg gcc tgc tct gat att cac att aat      385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
          115             120             125

gag tta atg ata atg ata att gga gca ctt gtt gtt ata ctt cca ttt      433
Glu Leu Met Ile Met Ile Ile Gly Ala Leu Val Val Ile Leu Pro Phe
          130             135             140

cta ctc atc ata gtg tct tat gcg cac att gtc tcc tcc att ctc aaa      481
Leu Leu Ile Ile Val Ser Tyr Ala His Ile Val Ser Ser Ile Leu Lys
          145             150             155

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct      529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
          165             170             175

cat ctg tct gcg gtg tca ctg ttc tat ggg tca gtc att gtt ctg tac      577
His Leu Ser Ala Val Ser Leu Phe Tyr Gly Ser Val Ile Val Leu Tyr
          180             185             190

tta tgt cca tca tct aat aac tct act gtg aag gat act gtc atg tct      625
Leu Cys Pro Ser Ser Asn Asn Ser Thr Val Lys Asp Thr Val Met Ser
          195             200             205

atg atg tac act gtg gtg act ccc      649
Met Met Tyr Thr Val Val Thr Pro
          210             215

<210> 415
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR7M; Accession DDBJ/EMBL/GenBank = AF073981

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<222> (1)..(649)
 <223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982

<220>
 <221> CDS
 <222> (2)..(649)
 <223> Product = olfactory receptor; region between transmembrane domains
 TM2 and TM7

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<400> 416
c ttc tct gat ctc tgc ttt tcc tct gtc aca atg ccc aaa ttg ctg cag      49
  Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
    1             5             10             15

aat ata cag agc cag gac cca tcc atc ccc tat gca ggc tgc ctg gca      97
Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
          20             25             30

caa aca tac ttc ttt atg gtt ttt gga gat atg gag agc ttc ctt ctt     145
Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
          35             40             45

gtg gcc atg gcc tat gac cgc tat gtg gcc atc tgc ttc cct ctg cat     193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
          50             55             60

tac acc agc atc atg agt ccc aaa ctc tgt ggt tgt cta atg ctg cta     241
Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
          65             70             75             80

ttg tgg atg cta aca aca tcc cat gcc atg atg cat act ctc ctt gca     289
Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
          85             90             95

gca aga ttg tct ttt tgt gag aac aat gtg atc ctc aat ttt ttc tgt     337
Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
          100            105            110

gac cta ttt gta ctc cta aag ctg gct tgc tca gac act tat gtt aat     385
Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
          115            120            125

gag ttg atg ata ttt ata atg agt tcc ctc ctc att gtt att cca ttt     433
Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe
          130            135            140

ttc ctc att gtc atg tct tat gca agg atc att gcc tcc att ctt aag     481
Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys
          145            150            155            160

gtt cca tct att caa ggg atc tac aag gtc ttc tcc acc tgt ggt tcc     529
Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser
          165            170            175

cat ctg tct gtg gtg acc ttg ttt tat ggg aca att att ggt ctc tac     577
His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
          180            185            190

tta tgt cca tca ggt aat aat tcc aca gta aag ggg act gtc atg gcc     625
Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala
          195            200            205

atg atg tac aca gcg gtg act ccc                                     649
Met Met Tyr Thr Ala Val Thr Pro
          210            215
  
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<210> 417
 <211> 216
 <212> PRT
 <213> Mus musculus domesticus

 <220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR8M; Accession DDBJ/EMBL/GenBank = AF073982

 <400> 417

Phe Ser Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
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Asn Ile Gln Ser Gln Asp Pro Ser Ile Pro Tyr Ala Gly Cys Leu Ala
 20 25 30

Gln Thr Tyr Phe Phe Met Val Phe Gly Asp Met Glu Ser Phe Leu Leu
 35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
 50 55 60

Tyr Thr Ser Ile Met Ser Pro Lys Leu Cys Gly Cys Leu Met Leu Leu
 65 70 75 80

Leu Trp Met Leu Thr Thr Ser His Ala Met Met His Thr Leu Leu Ala
 85 90 95

Ala Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Leu Asn Phe Phe Cys
 100 105 110

Asp Leu Phe Val Leu Leu Lys Leu Ala Cys Ser Asp Thr Tyr Val Asn
 115 120 125

Glu Leu Met Ile Phe Ile Met Ser Ser Leu Leu Ile Val Ile Pro Phe
 130 135 140

Phe Leu Ile Val Met Ser Tyr Ala Arg Ile Ile Ala Ser Ile Leu Lys
 145 150 155 160

Val Pro Ser Ile Gln Gly Ile Tyr Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ser Val Val Thr Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
 180 185 190

Leu Cys Pro Ser Gly Asn Asn Ser Thr Val Lys Gly Thr Val Met Ala
 195 200 205

Met Met Tyr Thr Ala Val Thr Pro

215

368

Variable	Mean	SD	Min	Max
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	1500	500	500	3000
Health status	0.8	0.2	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	0.7	0.3	0	1
Depression score	0.4	0.4	0	1
Life satisfaction	0.6	0.3	0	1
Quality of life	0.7	0.2	0	1
Healthcare utilization	0.5	0.5	0	1
Health insurance status	0.9	0.1	0	1
Healthcare access	0.8	0.2	0	1
Healthcare cost	1000	300	500	2000
Healthcare quality	0.7	0.2	0	1
Healthcare satisfaction	0.6	0.3	0	1
Healthcare utilization frequency	0.5	0.5	0	1
Healthcare utilization cost	500	200	250	1000
Healthcare utilization quality	0.7	0.2	0	1
Healthcare utilization satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost	250	100	125	500
Healthcare utilization frequency quality	0.7	0.2	0	1
Healthcare utilization frequency satisfaction	0.6	0.3	0	1
Healthcare utilization cost quality	0.7	0.2	0	1
Healthcare utilization cost satisfaction	0.6	0.3	0	1
Healthcare utilization quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality	0.7	0.2	0	1
Healthcare utilization frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency quality satisfaction	0.7	0.2	0	1
Healthcare utilization cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization cost frequency satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization frequency quality cost satisfaction	0.7	0.2	0	1
Healthcare utilization frequency quality cost satisfaction	0.6	0.3	0	1
Healthcare utilization cost frequency quality satisfaction	0.7	0.2	0	1
Healthcare utilization cost frequency quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.7	0.2	0	1
Healthcare utilization frequency cost quality satisfaction	0.6	0.3	0	1
Healthcare utilization quality frequency cost satisfaction	0.7	0.2	0	1
Healthcare utilization quality frequency cost satisfaction	0.6	0.3	0	1
Healthcare utilization frequency cost quality satisfaction	0.			

165

170

175

His Leu Ser Ile Val Ser Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
 180 185 190

Val Ser Ser Val Val Ile Gln Ser Ser His Ser Ala Ala Arg Ala Ser
 195 200 205

Val Met Tyr Thr Val Val Thr Pro
 210 215

<210> 420

<211> 646

<212> DNA

<213> Mus musculus domesticus

<220>

<221> misc_feature

<222> (1)..(646)

<223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank = AF073984

<220>

<221> CDS

<222> (2)..(646)

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 420

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 Ser Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
 1 5 10 15

att cac ata cta aga aat caa gcc att tgc ttc tct ggg tgc ctc aca 97
 Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
 20 25 30

cag ctg tat ttt ctc tgt gtg ttt gct gac atg gac aat ttc ctg ctg 145
 Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu
 35 40 45

gct gtg atg gcc tat gac cga ttt gtg gcc ata tgc cac cct tta cac 193
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60

tac aca aca aag atg acc cat cag ctt tgt gcc ttt ctt gtt gtt ggg 241
 Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly
 65 70 75 80

tcc tgg atg gta gcc agt ctg aat gct ctg ttg cac aca ctg ctc gtg 289
 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val
 85 90 95

gct caa ctc tac ttc tgt ggg gac aat gtg atc ccc cac ttc ttc tgt 337
 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110

gaa gtg act ccc ctg ctg aaa ctc tct tgc tca gac aca cat ctc aat 385
 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn
 115 120 125

gag ttg atg att ctt gct gtt gca ggg ctg ata atg tta gct cca ttt 433

370

09347151-08001
 106080-55724260

Glu Leu Met Ile Leu Ala Val Ala Gly Leu Ile Met Leu Ala Pro Phe
 130 135 140
 gtt tgc atc ctc ttg tct tat atc ctt att gct tgt gcc atc ctg aaa 481
 Val Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ala Cys Ala Ile Leu Lys
 145 150 155 160
 atc tca tcc aca gga aga tgg aaa gcc ttc tct acc tgt gcc tca cac 529
 Ile Ser Ser Thr Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His
 165 170 175
 ttg gct gtt gtg tgc ctc ttc tat gcc act atc ata tcc ctg tat ttc 577
 Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ser Leu Tyr Phe
 180 185 190
 aac ccc tca tct tct cac tca gct ggg agg gac atg gca gct gcc atg 625
 Asn Pro Ser Ser Ser His Ser Ala Gly Arg Asp Met Ala Ala Ala Met
 195 200 205
 atg tac aca gtg gtg acc ccc 646
 Met Tyr Thr Val Val Thr Pro
 210 215

<210> 421
 <211> 215
 <212> PRT
 <213> Mus musculus domesticus
 <220>
 <221> misc_feature
 <222> (1)..(646)
 <223> Taxon = 10092; clone = OR912-47M6; Accession DDBJ/EMBL/GenBank =
 AF073984

<400> 421
 Ser Val Asp Val Cys Phe Ser Ser Thr Thr Val Pro Lys Val Leu Ala
 1 5 10 15
 Ile His Ile Leu Arg Asn Gln Ala Ile Ser Phe Ser Gly Cys Leu Thr
 20 25 30
 Gln Leu Tyr Phe Leu Cys Val Phe Ala Asp Met Asp Asn Phe Leu Leu
 35 40 45
 Ala Val Met Ala Tyr Asp Arg Phe Val Ala Ile Cys His Pro Leu His
 50 55 60
 Tyr Thr Thr Lys Met Thr His Gln Leu Cys Ala Phe Leu Val Val Gly
 65 70 75 80
 Ser Trp Met Val Ala Ser Leu Asn Ala Leu Leu His Thr Leu Leu Val
 85 90 95
 Ala Gln Leu Tyr Phe Cys Gly Asp Asn Val Ile Pro His Phe Phe Cys
 100 105 110
 Glu Val Thr Pro Leu Leu Lys Leu Ser Cys Ser Asp Thr His Leu Asn


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115              120              125

Glu Leu Met Ile Leu Ala Val Ala Gly Leu Ile Met Leu Ala Pro Phe
130              135              140

Val Cys Ile Leu Leu Ser Tyr Ile Leu Ile Ala Cys Ala Ile Leu Lys
145              150              155              160

Ile Ser Ser Thr Gly Arg Trp Lys Ala Phe Ser Thr Cys Gly Ser His
165              170              175

Leu Ala Val Val Cys Leu Phe Tyr Gly Thr Ile Ile Ser Leu Tyr Phe
180              185              190

Asn Pro Ser Ser Ser His Ser Ala Gly Arg Asp Met Ala Ala Ala Met
195              200              205

Met Tyr Thr Val Val Thr Pro
210              215

<210> 422
<211> 650
<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/GenBank =
AF073985

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 422
c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag atg ctg gta      49
  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
   1              5              10              15

aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc      97
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
   20              25              30

cag atg tct gtc ttc ttg gtt ttt gga gaa ctg gac aac ttt ctc ctg      145
Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn Phe Leu Leu
   35              40              45

gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat      193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
   50              55              60

tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg      241
Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu
   65              70              75              80

tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gta      289

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Ser	Trp	Val	Val	Ser 85	Ile	Leu	His	Ala	Phe 90	Leu	Gln	Ser	Ser	Ile 95	Val	
cta Leu	cag Gln	ttg Leu	acc Thr 100	ttt Phe	tgt Cys	gga Gly	gat Asp	gta Val 105	aga Arg	att Ile	ccc Pro	cac His	ttc Phe 110	ttc Phe	tgt Cys	337
gag Glu	ctt Leu	aac Asn 115	cag Gln	ctg Leu	tct Ser	caa Gln	ctc Leu 120	aca Thr	tgt Cys	tca Ser	gac Asp	agc Ser 125	tta Leu	tca Ser	agc Ser	385
cac His	ctc Leu 130	ata Ile	atg Met	cat His	ctt Leu	gta Val 135	cct Pro	gtt Val	cta Leu	ttg Leu	gga Gly 140	gcc Ala	att Ile	tcc Ser	ttc Phe	433
agt Ser 145	agt Ser	atc Ile	ctt Leu	tac Tyr	tct Ser 150	tat Tyr	ttc Phe	aag Lys	ata Ile	gtg Val 155	tcc Ser	tcc Ser	ata Ile	tgt Cys	tct Ser 160	481
atc Ile	tcc Ser	tca Ser	gtt Val 165	caa Gln	ggg Gly	aag Lys	tac Tyr	aag Lys	gca Ala 170	ttt Phe	tct Ser	aca Thr	tgt Cys	gtc Val 175	tct Ser	529
cac His	ctt Leu	tcc Ser	att Ile 180	gta Val	tcc Ser	tta Leu	ttt Phe	tat Tyr 185	agt Ser	aca Thr	ggc Gly	ctt Leu	gga Gly 190	gtg Val	tat Tyr	577
gtc Val	agt Ser	tct Ser 195	gct Ala	gtg Val	gtc Val	caa Gln	agc Ser 200	tct Ser	cac His	tct Ser	gct Ala	gca Ala 205	aga Arg	gcc Ala	tct Ser	625
gtg Val	atg Met 210	tat Tyr	act Thr	gtg Val	gtc Val	aca Thr 215	cac His	g								650

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<210> 423
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(650)
<223> Taxon = 10092; clone = OR912-47M7; Accession DDBJ/EMBL/GenBank =
AF073985
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Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Met Leu Val
1 5 10 15

Gln Met Ser Val Phe Leu Val Phe Gly Glu Leu Asp Asn Phe Leu Leu
35 40 45

Tyr Thr Phe Ile Val Asn Gln His Leu Cys Ile Leu Met Val Leu Leu

[illegible]

```
<210> 424
<211> 649
<212> DNA
<213> Mus musculus domesticus
```

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<400> 424
c ttt gtg gac atc tgt ttc acc tcc acc act gtc cca aag gtg ctg gta 49
  Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Val Leu Val
   1             5             10             15

aat ata cag act caa agc aag gcc att aca tat gca gac tgt att agc 97
Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser
      20             25             30

cag atg tct gtc ttc ttg gtt ttt gca gaa ttg gac aac ttt ctg ctg 145

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05747153.030901

```

Gln Met Ser Val Phe Leu Val Phe Ala Glu Leu Asp Asn Phe Leu Leu
      35              40              45

gct gtg atg gcc tat gac cga tat gtg gct atc tgt cac cca ttg tat    193
Ala Val Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys His Pro Leu Tyr
      50              55              60

tac aca ttc att gtt aac caa cat ctc tgt ata ctg atg gtt ctg ctg    241
Tyr Thr Phe Ile Val Ser Ile Gln His Leu Cys Ile Leu Met Val Leu Leu
      65              70              75              80

tcc tgg gtt gtt agc atc cta cat gcc ttc tta cag agc tca att gtg    289
Ser Trp Val Val Ser Ile Leu His Ala Phe Leu Gln Ser Ser Ile Val
      85              90              95

cta cag ttg acc ttt tgt gga gat gta aaa att ccc cac ttc ttc tgc    337
Leu Gln Leu Thr Phe Cys Gly Asp Val Lys Ile Pro His Phe Phe Cys
      100             105             110

gag ctt aac cag ctg tct caa ctc aca tgt tta gac agc ttt tca agc    385
Glu Leu Asn Gln Leu Ser Gln Leu Thr Cys Leu Asp Ser Phe Ser Ser
      115             120             125

cac ctc ata atg aat ctt gta cct gtt cta ttg gca gtc att tcc ttc    433
His Leu Ile Met Asn Leu Val Pro Val Leu Leu Ala Val Ile Ser Phe
      130             135             140

agt agt atc ctt tac tct tat ttc aag ata gtg tcc tcc ata tgt tct    481
Ser Ser Ile Leu Tyr Ser Tyr Phe Lys Ile Val Ser Ser Ile Cys Ser
      145             150             155             160

atc tcc tca gtt caa ggg aag tac aag gca ttt tct aca tgt gtc tct    529
Ile Ser Ser Val Gln Gly Lys Tyr Lys Ala Phe Ser Thr Cys Val Ser
      165             170             175

cac ctt tcc att gtc ttc tta ttt tat agt aca ggc ctt gga gtg tat    577
His Leu Ser Ile Val Phe Leu Phe Tyr Ser Thr Gly Leu Gly Val Tyr
      180             185             190

gtc agt tct gct gtg gtc caa agc tct cac tct gct gca aga gcc tct    625
Val Ser Ser Ala Val Val Gln Ser Ser His Ser Ala Ala Arg Ala Ser
      195             200             205

gtg atg tat act gtg gtc acc ccg    649
Val Met Tyr Thr Val Val Thr Pro
      210             215

```

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<210> 425
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR912-47M8; Accession DDBJ/EMBL/GenBank =
AF073986

```

<400> 425

```

Phe Val Asp Ile Cys Phe Thr Ser Thr Thr Val Pro Lys Val Leu Val
1              5              10              15

```

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Asn Ile Gln Thr Gln Ser Lys Ala Ile Thr Tyr Ala Asp Cys Ile Ser

```

[illegible]

```
<210> 426
<211> 649
<212> DNA
<213> Mus musculus domesticus
```

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<220>
<221> CDS
<222> (2) .. (649)
```

<223> Product = olfactory receptor; region between transmembrane domains TM2 and TM7

<400> 426

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c ttt gca gat ctc tgc ttt tct act acc aca gtg ccc cag gtg ctt gtc      49
  Phe Ala Asp Leu Cys Phe Ser Thr Thr Val Pro Gln Val Leu Val
    1             5             10             15

cac ttc ctg gtg aag agg aag acc att tct ttt gct gga tgt tct aca      97
His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr
    20             25             30

cag ata gtg gtg ttg ctt ctg gtc gga tgc aca gag tgt gca ctg ctg      145
Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu
    35             40             45

gca gtg atg tcc tat gac cga tat gtg gct gtc tgc aaa cct ctg cac      193
Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His
    50             55             60

tac tcc acc atc atg aca cac tgg cta tgt gtt cag ctg gct gca ggg      241
Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly
    65             70             75             80

tcc tgg gcc agt ggt gca ctt gtg tcc ctg gtg gat acc aca ttc aca      289
Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr
    85             90             95

tta cgt ctt cct tat cga gga aac aat gtc att aac cac ttt ttc tgt      337
Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys
    100            105            110

gaa cct cct gcc ctc ctg aag ctg gca tgc gca gat aca tac agc aca      385
Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr
    115            120            125

gag atg gcg atc ttt gca atg ggt gtg gta atc ctc cta gca cct gtc      433
Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val
    130            135            140

tcc ctc atc ctc acc tcc tac tgg aac atc atc tcc act gta atc cag      481
Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln
    145            150            155            160

atg cag tct ggg gaa gga agg ctc aag gtc ttc tcc acc tgt ggc tcc      529
Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser
    165            170            175

cac ctc att gtt gtt gtt ctc ttc tac ggc tca gca ata ttt gcc tac      577
His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr
    180            185            190

atg agg ccc aac tct aag ata atg aat gaa aag gat aaa atg att tgc      625
Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser
    195            200            205

gtg ttc tat tca gca gtg acc ccg      649
Val Phe Tyr Ser Ala Val Thr Pro
    210            215

```

<210> 427

<211> 216

<212> PRT

<213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(649)
 <223> Taxon = 10092; clone = OR912-47M9; Accession DDBJ/EMBL/GenBank = AF073987

<400> 427

Phe Ala Asp Leu Cys Phe Ser Thr Thr Thr Val Pro Gln Val Leu Val
 1 5 10 15

His Phe Leu Val Lys Arg Lys Thr Ile Ser Phe Ala Gly Cys Ser Thr
 20 25 30

Gln Ile Val Val Leu Leu Leu Val Gly Cys Thr Glu Cys Ala Leu Leu
 35 40 45

Ala Val Met Ser Tyr Asp Arg Tyr Val Ala Val Cys Lys Pro Leu His
 50 55 60

Tyr Ser Thr Ile Met Thr His Trp Leu Cys Val Gln Leu Ala Ala Gly
 65 70 75 80

Ser Trp Ala Ser Gly Ala Leu Val Ser Leu Val Asp Thr Thr Phe Thr
 85 90 95

Leu Arg Leu Pro Tyr Arg Gly Asn Asn Val Ile Asn His Phe Phe Cys
 100 105 110

Glu Pro Pro Ala Leu Leu Lys Leu Ala Ser Ala Asp Thr Tyr Ser Thr
 115 120 125

Glu Met Ala Ile Phe Ala Met Gly Val Val Ile Leu Leu Ala Pro Val
 130 135 140

Ser Leu Ile Leu Thr Ser Tyr Trp Asn Ile Ile Ser Thr Val Ile Gln
 145 150 155 160

Met Gln Ser Gly Glu Gly Arg Leu Lys Val Phe Ser Thr Cys Gly Ser
 165 170 175

His Leu Ile Val Val Val Leu Phe Tyr Gly Ser Ala Ile Phe Ala Tyr
 180 185 190

Met Arg Pro Asn Ser Lys Ile Met Asn Glu Lys Asp Lys Met Ile Ser
 195 200 205

Val Phe Tyr Ser Ala Val Thr Pro
 210 215

<210> 428
 <211> 649

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<212> DNA
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<220>
<221> CDS
<222> (2)..(649)
<223> Product = olfactory receptor; region between transmembrane domains
TM2 and TM7

<400> 428
c ttc act gac ctc tgc ttt tcc tct gtc aca atg ccc aag ttg ctg cag      49
  Phe Thr Asp Leu Cys Phe Ser Ser Val Thr Met Pro Lys Leu Leu Gln
   1             5             10             15

aac atg cag agc caa gtt cct tca atc ccc tat gca ggc tgc ctg aca      97
Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
   20             25             30

caa atg tac ttc ttt ttg ttt ttt gga gat ctt gag agc ttc ctc ctt     145
Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
   35             40             45

gtg gcc atg gcc tat gac cga tat gta gcc atc tgc ttc cct ctt cat     193
Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
   50             55             60

tac acc agc att atg agc ccc agg ctc tgt gtg agt ctt gtg ctg ctg     241
Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
   65             70             75

tcc tgg ttg ctg acc atg tcc cat tcc atg ctg cac act ttg ctc tta     289
Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
   85             90             95

act agg ttg tct ttc tgt gaa aac aat gtg atc ccc cat ttt ttc tgt     337
Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
  100             105             110

gat ctg tct gct ctg ctg aag ctg gcc tgc tct gat att cac att aat     385
Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
  115             120             125

gaa ttg gtg ata ttg atc ata gga ggg ctt gtt gtt ata ctt cca ttt     433
Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
  130             135             140

cta ctc gtc aca gtg tct tat gca cgc atc atc tcc tcc att ctc aag     481
Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
  145             150             155

gtc cct tca act cga ggc atc cac aag gtc ttc tcc act tgt ggt tct     529
Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
  165             170             175

cac ctg tct gtg gtg tca ctg ttc tat ggg aca att att ggc ctc tac     577
His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
  180             185             190

tta tgt cca tct gct aat aac tct act cta aag gac act gtc atg tct     625
Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
  195             200             205

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[illegible]

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<210> 429
<211> 216
<212> PRT
<213> Mus musculus domesticus

<220>
<221> misc_feature
<222> (1)..(649)
<223> Taxon = 10092; clone = OR9M; Accession DDBJ/EMBL/GenBank = AF073988

<400> 429
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Asn Met Gln Ser Gln Val Pro Ser Ile Pro Tyr Ala Gly Cys Leu Thr
20 25 30

Gln Met Tyr Phe Phe Leu Phe Phe Gly Asp Leu Glu Ser Phe Leu Leu
35 40 45

Val Ala Met Ala Tyr Asp Arg Tyr Val Ala Ile Cys Phe Pro Leu His
50 55 60

Tyr Thr Ser Ile Met Ser Pro Arg Leu Cys Val Ser Leu Val Leu Leu
65 70 75 80

Ser Trp Leu Leu Thr Met Ser His Ser Met Leu His Thr Leu Leu Leu
85 90 95

Thr Arg Leu Ser Phe Cys Glu Asn Asn Val Ile Pro His Phe Phe Cys
100 105 110

Asp Leu Ser Ala Leu Leu Lys Leu Ala Cys Ser Asp Ile His Ile Asn
115 120 125

Glu Leu Val Ile Leu Ile Ile Gly Gly Leu Val Val Ile Leu Pro Phe
130 135 140

Leu Leu Val Thr Val Ser Tyr Ala Arg Ile Ile Ser Ser Ile Leu Lys
145 150 155 160

Val Pro Ser Thr Arg Gly Ile His Lys Val Phe Ser Thr Cys Gly Ser
165 170 175

His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Ile Ile Gly Leu Tyr
180 185 190

Leu Cys Pro Ser Ala Asn Asn Ser Thr Leu Lys Asp Thr Val Met Ser
 195 200 205

Leu Met Tyr Thr Val Val Thr Pro
 210 215

<210> 430
 <211> 1865
 <212> DNA
 <213> Mus musculus domesticus

<220>
 <221> misc_feature
 <222> (1)..(1865)
 <223> Taxon = 10090; clone = OR1-72M13; cell line = NIH3T3; Accession
 DDBJ/EMBL/genBank = AF073989

<220>
 <221> CDS
 <222> (547)..(1482)
 <223> Product = olfactory receptor; orthologous to human gene OR1-72

<400> 430
 ctgcagagtg agttctagga cagccaggac tacacagaga aacctgaat caaaataaaa 60
 taaaataaaa tacaatagaa taaaataaaa taaacaaaaa agaaaaaaga agataaagat 120
 gtctaagaga agaattgagat ttcaaaagga atggatacag agaaggatg gtcatattca 180
 cagagacctt tctgaatgat cagaacttag tgtaaccact gaaaaatgtt gagaagtga 240
 gttggaaatc agagttgatc catcataaag gattacagca cttttagaaa ctgactgctt 300
 tgatctaaca cttccagagg ttatctgggtc ttcatgtggt ttaaaatttg tagagttagc 360
 agttctaagt agagataagg tagagaaact aataatgatg agaaaatgca ggattcctaa 420
 tttttattgt aataaaagct ttatgtacag ttattccaac acataaaagg acagagacct 480
 tagagactgt agtgtatgtt cctcaatctt tctctccagt aggtgtctag cttatttgtc 540
 aacaac atg aaa cca gaa aac caa aca aaa tat ttt aga att ttt gct 588
 Met Lys Pro Glu Asn Gln Thr Lys Tyr Phe Arg Ile Phe Ala
 1 5 10
 tct ggg gtt ttc caa tat cca gag cat caa ccc atg cta ttt gga ctg 636
 Ser Gly Val Phe Gln Tyr Pro Glu His Gln Pro Met Leu Phe Gly Leu
 15 20 25 30
 ttt ctg ctg atg ttt gtg gtc gct gtg ctt ggg aat ctt ctg atc att 684
 Phe Leu Leu Met Phe Val Val Ala Val Leu Gly Asn Leu Leu Ile Ile
 35 40 45
 ctg gcc gtc agc att gac tct cac ctg cat act ccc atg tac ttc ttt 732
 Leu Ala Val Ser Ile Asp Ser His Leu His Thr Pro Met Tyr Phe Phe
 50 55 60
 cta tct aac ctg tcc ttt tct gac att ggt ttc atc tct aca act gtc 780
 Leu Ser Asn Leu Ser Phe Ser Asp Ile Gly Phe Ile Ser Thr Thr Val
 65 70 75
 cct aag atg ttg gtg aat atc caa aca cag agc aag tcc atc tcc tat 828
 Pro Lys Met Leu Val Asn Ile Gln Thr Gln Ser Lys Ser Ile Ser Tyr
 80 85 90

gca gaa tgc atc acc cag att tat ttt ttc atg ctc ttt gga ggc atg Ala Glu Cys Ile Thr Gln Ile Tyr Phe Phe Met Leu Phe Gly Gly Met 95 100 105 110	876
gac aca ctt ctc ctc acc gtg atg gcc tat gac cga ttt gtg gcc atc Asp Thr Leu Leu Leu Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile 115 120 125	924
tgt cac cca ctt cac tat tca gtc att atg aat cct caa cta agt ggt Cys His Pro Leu His Tyr Ser Val Ile Met Asn Pro Gln Leu Ser Gly 130 135 140	972
ttg cta gtt ctt gta tca tgg ttt att agc ttt tca tat tct ctg ata Leu Leu Val Leu Val Ser Trp Phe Ile Ser Phe Ser Tyr Ser Leu Ile 145 150 155	1020
cag agt cta ttg atg ctg cgg ttg tcc ttc tgt aca aat cag ata att Gln Ser Leu Leu Met Leu Arg Leu Ser Phe Cys Thr Asn Gln Ile Ile 160 165 170	1068
aaa cac ttt tac tgt gaa tat gcc aaa gcc ctc act ata gcc tgc tca Lys His Phe Tyr Cys Glu Tyr Ala Lys Ala Leu Thr Ile Ala Cys Ser 175 180 185 190	1116
gat aca cta atc aat cat atc ctt ctt tat att gtg ata tgg gtc ctt Asp Thr Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu 195 200 205	1164
ggc ttc atc cct ttc tca ggg atc ctt tat tca tac tat aaa att ttt Gly Phe Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe 210 215 220	1212
tct tca att ttg aga att cca tca aca gat gga aaa tat aaa gca ttt Ser Ser Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe 225 230 235	1260
tct acc tgt ggg tct cat cta tgc gtg gtt tct tta ttc tat ggg aca Ser Thr Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr 240 245 250	1308
ggc ctt agt gtg tac ctt agt tct gat gct act tcc tcc tct ggg aag Gly Leu Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys 255 260 265 270	1356
ggc gtg gtg gcc tca gta atg tat aca gtg gtc acc ccc atg ctg aac Gly Val Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn 275 280 285	1404
cct ttc atc tac agc ttg agg aac aaa gac att aag aag gcc tta aaa Pro Phe Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys 290 295 300	1452
aca ctt ggg aga ata ctt ctt tta aag tga taatttcaact ggttttagac Thr Leu Gly Arg Ile Leu Leu Leu Lys 305 310	1502
atctgaactg atagaaataa aatagtgaac taaagaaatt ctgtactata atcatgtaga	1562
aattttatcc agtttggttg tctatctttg attaaaatta tactgtgaat atttctatct	1622
gaaattttcta tgaatgctcc ttttttatcc gaagtctctt gtctcctccc ctgttttata	1682
cgacatatatt ctttacttca gtacaaagtc tacatttcag catgccaata taaccattca	1742
aataccaatt catgaattgt ttagtaaaag ttatgcaatg gctcatttac agaaagtcca	1802

Leu Ile Asn His Ile Leu Leu Tyr Ile Val Ile Trp Val Leu Gly Phe
195 200 205

Ile Pro Phe Ser Gly Ile Leu Tyr Ser Tyr Tyr Lys Ile Phe Ser Ser
210 215 220

Ile Leu Arg Ile Pro Ser Thr Asp Gly Lys Tyr Lys Ala Phe Ser Thr
225 230 235 240

Cys Gly Ser His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Leu
245 250 255

Ser Val Tyr Leu Ser Ser Asp Ala Thr Ser Ser Ser Gly Lys Gly Val
260 265 270

Val Ala Ser Val Met Tyr Thr Val Val Thr Pro Met Leu Asn Pro Phe
275 280 285

Ile Tyr Ser Leu Arg Asn Lys Asp Ile Lys Lys Ala Leu Lys Thr Leu
290 295 300

Gly Arg Ile Leu Leu Leu Lys
305 310